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Hamud, Fozia  
Wednesday, February 27, 2002 8:47 AM  
STIC-Biotech/ChemLib  
search for 09/617,720

Please search SEQ ID NO:1 from 310 to 2562 against commercial data bases and interference data bases. Thanks.

Fozia Hamud  
Art Unit 1647  
Crystal-Mall-One, Room 10Bo5  
308-8891  
mail Box: CM110C01

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FEB 27 2002  
STIC

of Contact:  
Sheppard

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## TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Other (specify): \_\_\_\_\_



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REFERENCE 1 (bases 1 to 2613)  
AUTHORS Barton,J.L., Herbst,R., Bosio,D., Higgins,L. and Nicklin,M.J.  
TITLE A tissue specific IL-1 receptor antagonist homolog from the IL-1  
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities  
Eur. J. Immunol. 30 (11), 3299-3308 (2000)  
20545212  
REFERENCE 2 (bases 1 to 2613)  
AUTHORS Nicklin,M.J.  
TITLE Direct Submission  
JOURNAL Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and  
Genetic Medicine, University of Sheffield, Royal Hallamshire  
Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM  
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DEFINITION AX092420  
ACCESSION AX092420  
VERSION AX092420.1 GI:13444524  
KEYWORDS human.

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## RESULT 5

AX080431 6540 bp DNA PAT 22-FEB-2001  
LOCUS AX080431  
DEFINITION Sequence 43 from Patent WO0105974.  
ACCESSION AX080431  
VERSION AX080431.1 GI:13159871

## KEYWORDS

human.  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 6540)

AUTHORS Nicklin,M. and Barton,J.

JOURNAL The 11-111 gene and polypeptide products

PATENT: WO 0105974-A 43 25-JAN-2001;

Interleukin Genetics, Inc. (US)

ATTN: Location/Qualifiers

1. 6540

/organism="Homo sapiens"

BASE COUNT 1747 a 1458 c 1709 g 1626 t

ORIGIN

Query Match 97.5%; Score 2195.6; DB 6; Length 6540;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 2237; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

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1-6.  
ACCESSION AJ271338  
VERSION AJ271338.1 GI:6729586  
KEYWORDS IL1L1 gene; interleukin-1 like protein 1.

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 6540)  
AUTHORS Barton,J.L., Herbst,R., Bosisio,D., Higgins,L. and Nicklin,M.J.  
TITLE A tissue specific IL-1 receptor antagonist homolog from the IL-1  
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities  
JOURNAL Eur. J. Immunol. 30 (11), 3299-3308 (2000)  
MEDLINE 20545212  
REFERENCE 2 (bases 1 to 6540)  
AUTHORS Nicklin,M.J.H.  
TITLE Direct Submission  
JOURNAL Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and  
Genetic Medicine, University of Sheffield, Royal Hallamshire  
Hospital, Sheffield, South Yorkshire, UNITED KINGDOM  
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

TITLE	The sequence of Homo sapiens clone
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 197308)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (04-DEC-1999) Genome Sequencing Center, Washington

REFERENCE 3 (bases 1 to 197308)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-JUL-2001) Genome Sequencing Center, Washington

ENT On Jul 14, 2001 this sequence version replaced gl:13431151.

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WGS05C  
 Web site: <http://genome.wustl.edu/gsc/index.shtml>  
 ----- Project Information -----  
 Center project name: H.NH0339F22

FEATURES	Location/Qualifiers
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ACCESSION AF216693
VERSION AF216693.1 GI:8572054
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 7604)
Muller, J.J., Nelken, S.T. and Ford, J.E.
Organization of the human Interleukin-1 receptor antagonist gene
IL1HY1
JOURNAL Immunogenetics 51 (6), 425-428 (2000)
MEDLINE 20322477
REFERENCE 2 (bases 1 to 7604)
Muller, J.J., Nelken, S.T. and Ford, J.E.
Direct Submission
Submitted (15-DEC-1999) Functional Genomics, HYSEQ Inc, 670 Almenor
Ave., Sunnyvale, CA 94086, USA
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BASE COUNT 2079 a 1647 c 1865 g 2008 t 5 others
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[illegible]



RESULT 9  
LOCUS AX069311 7605 bp DNA PAT 25-JAN-2001  
DEFINITION Sequence 8 from Patent WO0102571.  
ACCESSION AX069311  
VERSION AX069311.1 GI:12579183  
KEYWORDS  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 7605)  
AUTHORS Ford, J. and Pace, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: WO 0102571-A 8 11-JAN-2001;  
HISEQ, INC. (US)  
FEATURES  
source Location/Qualifiers  
1..7605  
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/db\_xref="taxon:9606"  
BASE COUNT 2079 a 1647 c 1865 g 2009 t 5 others  
ORIGIN  
Query Match 96.8%; Score 2180.4; DB 6; Length 7605;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2234; Conservative 0; Mismatches 16; Indels 4; Gaps 4;  
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QY 121 ccagcttcacagaaatgtgtgctgaatgcccccaacacacagactctacttccagact 180  
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QY 1440 tgaatctcagctgt 1499  
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D	E	F	VERSION AX069309.1 GI:12579181	
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D	E	F	ORGANISM Homo sapiens	
D	E	F	REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
D	E	F	AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
D	E	F	TITLE 1 (bases 1 to 2648)	
D	E	F	JOURNAL Ford,J. and Pace,A.	
D	E	F	FIGURE A interleukin-1 receptor antagonist and uses thereof	
D	E	F	PATENT Patent: WO 0102571-A 6 11-JAN-2001;	
D	E	F	HYSEQ, INC. (US)	
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 Db 1102 CCCACCCCTTCCCTTAAATCCGACACTGTGATATGCTACCTTCTTATCTTCCCTC 1161  
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 Db 2302 CCTGTCTCTCTGTGTATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2361  
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 ACCESSION AK002125  
 VERSION AK002125.1 GI:7023811  
 KEYWORDS oligo capping; f1s (full insert sequence).  
 SOURCE Homo sapiens; placenta cDNA to mRNA, clone lib:PLACE1  
 Clone:PLACE1009110.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (sites)  
 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,  
 Wagatsuma,M., Hosoliri,T., Kaku,Y., Kodaira,H., Kondo,H.,  
 Sugawara,M., Takahashi,M., Ishida,S., Ishida,S., Murakawa,K.,  
 Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,  
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,  
 Nakamura,Y., Nagahari,K., Masuno,Y., Ninomiya,K. and Iwayanagi,T.  
 NEDO human cDNA sequencing project

TITLE

JOURNAL Unpublished (2000)  
REFERENCE 2 (bases 1 to 1866)  
AUTHORS Isogai,T. and Otsuki,T.  
TITLE Direct Submission  
JOURNAL Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisaizau, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)  
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.  
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VERSION			
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REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 5751)		
FEATURES	Ford, J. and Pace, A.		
source	A interleukin-1 receptor antagonist and uses thereof		
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ACCESSION AF201830  
VERSION AF201830.1 GI:6694387  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1288)  
Smith,D.E., Kenschaw,B.R., Ketchum,R.R., Kubin,M., Garika,K.E. and  
Slms,J.E.  
Four new members expand the interleukin-1 superfamily  
J. Biol. Chem. 275 (2), 1169-1175 (2000)  
2 (bases 1 to 1288)  
Slms,J.E.  
Direct Submission  
Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51  
University Street, Seattle, WA 98101, USA  
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ACCESSION AX069305  
VERSION AX069305.1 GI:12579177  
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SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 985)  
Ford,J. and Pace,A.  
A Interleukin-1 receptor antagonist and uses thereof  
Patent: WO 0102571-A 2 11-JAN-2001;  
HYSEO, INC. (US)  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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5	2180.4	96.8	7605	22	AAAF31356
6	2178.4	96.7	2647	22	AAAF31354
7	2178.4	96.7	2648	20	AAZ30051
8	2020.6	89.7	2490	21	AAH50813
9	1835	81.4	1866	22	AAH15099
10	1577.6	70.0	5751	22	AAAF31355
11	1566.6	69.5	5752	20	AAZ30052

12	933.2	41.4	1323	21	AAZ50812	Human TANGO-93 cDN
13	886.2	39.3	985	22	AAAF31352	B2HFLS20W cDNA 11b
14	886.2	39.3	1282	22	AAAF31353	Extension of B2HFL
15	885.2	39.3	1282	20	AAZ30050	cDNA encoding a hu
16	883.6	39.2	985	20	AAZ30049	cDNA encoding a hu
17	641	28.5	1025	22	AAAD12295	Human Interleukin-
18	527.8	23.4	555	22	AAH07999	Human cDNA clone (
19	380.8	16.9	416	22	AAH12965	Human CDNA clone (
20	354.6	15.7	766	21	AAA09193	Human IL-1 homolo
21	230	10.2	357	22	AAAF31351	B2HFLS20W cDNA 11b
22	222.8	9.9	358	20	AAZ30048	cDNA encoding a hu
23	188	8.3	468	20	AAH89432	Human Interleukin
24	188	8.3	468	21	AAAS1597	Human IL-1 recepto
25	159.2	7.1	475	22	AAI05083	Probe #5074 used t
26	156.4	6.9	1275	21	AAA09198	Murine IL-1 homolo
27	156.4	6.9	1284	22	AAAF27924	Murine IL-11 codi
28	156.4	6.9	1360	21	AAZ50811	Murine TANGO-93 cD
29	156.4	6.9	1385	21	AAAS1599	Murine IL-1 recept
30	154.8	6.3	8032	22	AAAF31372	Invention related
31	141.6	6.3	468	22	AAAF31373	Invention related
32	141.6	6.3	468	22	AAAC81700	Murine Interleukin
33	140.6	6.2	470	19	AAV71958	Rodent Interleukin
34	138.6	6.2	468	20	AAH89431	Mouse Interleukin
35	135	6.0	465	21	AAA09194	Human IL-1 homolo
36	132.2	5.9	465	21	AAA09195	Human IL-1 homolo
37	128	5.7	590	22	AAI19031	Probe #8964 for ge
38	128	5.7	590	22	AAI14171	Probe #12857 used
39	125	5.5	936	22	AAAF58252	Oligonucleotide D1
40	125	5.5	936	22	AAAF58254	Oligonucleotide D1
41	125	5.5	936	22	AAAF58257	Oligonucleotide D1
42	125	5.5	936	22	AAAF58259	Oligonucleotide D2
43	125	5.5	936	22	AAAF58262	Oligonucleotide D2
44	125	5.5	938	22	AAAF58255	Oligonucleotide D1
45	123.6	5.5	1731	20	AAZ98008	Human secreted pro

#### ALIGNMENTS

RESULT 1	
ID AAF27921	standard; cDNA; 2562 BP.
XX	
AC AAF27921:	
XX	
DT 08-MAY-2001	(first entry)
XX	
DE Human IL-IL1 coding sequence.	
XX	
KW Human: IL-IL1; Interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;	
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;	
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;	
KW osteoporosis; systemic lupus erythematosus; ss.	
XX	
OS Homo sapiens.	
XX	
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FT CDS	30..497
FT	/*tag= a
FT	/product= "IL-IL1"
FT	/note= "this region is specifically claimed"
XX	
PN WO200105974-A2.	
XX	
PD 25-JAN-2001.	
XX	
PF 17-JUL-2000; 2000MO-US19508.	
XX	
PR 16-JUL-1999; 99US-0144298.	
XX	
PA (INTE-) INTERLEUKIN GENETICS INC.	
XX	
PI Nicklin M, Barton J;	

XX WPI: 2001-091974/10.  
XX Nucleic acids encoding human and murine interleukin-1L1 polypeptides  
PT useful for controlling inflammatory processes -  
XX  
PS Claim 12: Fig 1: 150pp: English.  
CC The present invention provides the protein and coding sequences of the  
CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is  
CC located between the IL-1beta and IL-1receptor genes at human chromosome  
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment  
CC of heart disease, cancer and inflammatory diseases such as rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,  
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,  
CC severe periodontal disease and pregnancy complications. The present  
CC sequence is the human IL-1L1 coding sequence.  
XX  
XX Sequence 2562 BP: 678 A: 579 C: 635 G: 670 T: 0 other:  
50  
Every Match 100.0%: Score 2253: DB 22: Length 2562:  
Best Local Similarity 100.0%: Pred. No. 0:  
Matches 2253: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
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DB 310 aatccaagagcttcaaccttctacccgaggaatgagagctacacctcagagtcgagtcg 369  
QY 61 ctgctacacgggctggtctctctgcaacggtgctgaaagccgatacagctgtcaagctca 120  
DB 370 ctgctacacgggctggtctctctgcaacggtgctgaaagccgatacagctgtcaagctca 429  
QY 121 cccagctcccgagaaatgctgctgaatgctcccccacacagacttctacttccagcagt 180  
DB 430 cccagctcccgagaaatgctgctgaatgctcccccacacagacttctacttccagcagt 489  
QY 181 gtgactaaggcaacgtgctcccccagaaatcccttggcagagccagctcggtgaggggt 240  
DB 490 gtgactaaggcaacgtgctcccccagaaatcccttggcagagccagctcggtgaggggt 549  
QY 241 gagtgagaggaacacatgagtgaggaacatctcttctgctctcagagcccccagctcga 300  
DB 550 gagtgagaggaacacatgagtgaggaacatctcttctgctctcagagcccccagctcga 609  
QY 301 ctatgtgagcaccgtgacacacttgtctctctgcttccaggttgcataaattctgagatt 360  
DB 610 ctatgtgagcaccgtgacacacttgtctctctgcttccaggttgcataaattctgagatt 669  
QY 361 ggaagctcaagctccagggctctcccccacatgagtgagtgactgctgtggaacctgtaaa 420  
DB 670 ggaagctcaagctccagggctctcccccacatgagtgagtgactgctgtggaacctgtaaa 729  
QY 421 accgtctgaggtaaacgtggaatacagaaagattctcttggggggtggggggag 480  
DB 730 accgtctgaggtaaacgtggaatacagaaagattctcttggggggtggggggag 789  
QY 481 tgcctggaataatctcctcttaataatgtaacagtgataccttgagcccgagagcc 540  
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DB 850 aaccatccacagttgagccttataaggtcagtagcttccacatgaaagctctctacac 909  
QY 601 accactgagcagagagagagtggtcataagatcagagatctatgaccttgagccagc 660  
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DB 970 cccacccctctctcttctcctgcaatgataatgtaacattcctatctctcccca 1029

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DB 1150 cagatgctgctctctctccatgtaaaagtgtcctatgacatgataagaaagctacta 1209  
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QY 961 tagaaaaaagctctggaagaagttacttcaattgtagcaatgctcaggtgtgtgcagata 1020  
DB 1270 tagaaaaaagctctggaagaagttacttcaattgtagcaatgctcaggtgtgtgcagata 1329  
QY 1021 ggtgatttctctttaaattctgtaattatctgtaattcttcttcttcttcttcttcttct 1080  
DB 1330 ggtgatttctctttaaattctgtaattatctgtaattcttcttcttcttcttcttcttct 1389  
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DB 1390 atgaattctctgtataaataaagaagaataatctatctgaggtgaagcagagacat 1449  
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DB 1930 tggagatttctgagcagacagagcttaagaaacacagagatgtgtgcaacatcagaagctt 1989  
QY 1681 ggaagagacag 1740  
DB 1990 ggaagagacag 2049  
QY 1741 ccttaatctcagacttccagctctcctggaacagaaagaaataaatttctggtgtgttttaag 1800  
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QY 1801 ccaccaagataatgtgttaacagagctctaggaataactatacagctgtctaaatgatcc 1860

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Db 2170 cgtctcccggttcttaacttctgtgtgtgtgtccctcccaatactgataagttgtctt 2229
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## RESULT 2

AAf92133 standard; cDNA; 2598 BP.

AAf92133;

15-MAY-2001 (first entry)

Human PRO342 cDNA.

Human; PRO protein; mapping; ss.

Homo sapiens.

WO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US23328.

01-SEP-1999; 99WO-US20111.

15-SEP-1999; 99WO-US21090.

07-DEC-1999; 99US-0169495.

09-DEC-1999; 99US-0170262.

11-JAN-2000; 2000US-0175481.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04342.

01-MAR-2000; 2000WO-US04414.

03-MAR-2000; 2000US-0187202.

25-APR-2000; 2000US-0199397.

22-MAY-2000; 2000WO-US14042.

05-JUN-2000; 2000US-0209832.

(GETH ) GENENTECH INC.

Eaton DJ, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,

Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI.

WPI: 2001-183260/18.

P-PSDB: AAB87601.

Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

Claim 2: Fig 151: 278bp; English.

The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 other;

Query Match 97.9%; Score 2205.2; DB 22; Length 2598;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2243; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

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Db 467 cccagcttccgaggaatggtgtgctggaatgcccacatcagaacttacttccagcagt 526
Qy 181 gtgactagaggaagcagtgcccccccaagaactccctgtgagcagacagctcgggtgaaagg 240
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Qy 241 gagtggagagagaccacatgagcgaacatcacttctgtcctcagaagcccccaggtctga 300
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Qy 361 gagactcagttcagaaggtctctcccccagatgagtgctcgtgtgaaacttctgaataa 420
Db 706 gagactcagttcagaaggtctctcccccagatgagtgctcgtgtgaaacttctgaataa 765
Qy 421 accatgtgggttaaacctgaggaatacagaagaattctgttgggggtggtggtggggg 480
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QY 1080 gatgaattctctgtataaaaaaagaagaataatbaatcttgaggtagaagcagagaca 1139
Db 1426 gatgaattctctgtataaaaaaagaagaataatbaatcttgaggtagaagcagagaca 1485
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QY 1620 atcgaagtttgcagcccaagcttaagaacacccaagatgtgccaacatacagaagct 1679
Db 1966 atcgaagtttgcagcccaagcttaagaacacccaagatgtgccaacatacagaagct 2025
QY 1680 tggaaagagcaagaagaatctctcccaagagcttgaagggataacgcgtcgtcgaa 1739
Db 2026 tggaaagagcaagaagaatctctcccaagagcttgaagggataacgcgtcgtcgaa 2085
QY 1740 accttaatctcagactccagctctcgtgaacgaagaagaataattcggctgtttaa 1799
Db 2086 accttaatctcagactccagctctcgtgaacgaagaagaataattcggctgtttaa 2145
QY 1800 gccaccaagaataattgtttacagagctctagaagaataatacagctgtcctaaatgatc 1859
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Db 2325 aagaactgcagacttctacttgaagcctctctctctgcacacacgcgcccaactatc 2384
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Db 2385 ttggtcactcgtcctcgtgggaagctagctgcacatctatgaagcaggtataagaagac 2444
QY 2100 ttacgtgttaaaaaatgaagctctcgtccacagccacatgaatgaacctagaagcagag 2159
Db 2445 ttacgtgttaaaaaatgaagctctcgtccacagccacatgaatgaacctagaagcagag 2504
QY 2160 actcgtgagataatcgatgtttgtgttttaagtgtgctcagtttggcttaactgtta 2219
Db 2505 actcgtgagataatcgatgtttgtgttttaagtgtgctcagtttggcttaactgtta 2564
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Db 2565 tgcagcaataaataataatgcagagaagaag 2598
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RESULT 3  
AAF27950  
ID AAF27950 standard; DNA; 6540 BP.

XX AAF27950;

DT 08-MAY-2001 (first entry)

XX Interleukin-IL1 genomic sequence.

Human: IL-1L1; Interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
Chromosome 2q13; Inflammatory disease; heart disease; Graves' disease;  
Rheumatoid arthritis; Inflammatory bowel disorder; diabetes; cancer;  
osteoporosis; systemic lupus erythematosus; ds.

XX Unidentified.

PN WO200105974 -A2.

XX 25-JAN-2001.

PF 17-JUL-2000; 2000WO-US19508.

XX 16-JUL-1999; 99US-0144298.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Nicklin M, Barton J;

PI WPI: 2001-091974/10.

XX Nucleic acids encoding human and murine Interleukin-IL1 polypeptides  
PT useful for controlling inflammatory processes -

PS Examples; Fig 11: 150pp; English.

XX The present invention provides the protein and coding sequences of the  
CC human and murine Interleukin-IL1 (IL-1L1) proteins. The IL-1L1 gene is  
CC located between the IL-1beta and IL-1receptor genes at human chromosome  
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment  
CC of heart disease, cancer and inflammatory diseases such as rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,



Oy	2040	ttggctcactgcgtctcgggggaagctagctgcacatgctcatalgacagagcctaataagagac	2099
Db	6309	ttggctcactgcgtctcgggggaagctagctgcacatgctcatalgacagagcctaataagagac	6368
Oy	2100	tttagtggtaaaataatgaagctctccggcccaagccacatagtagaaccttagaagacgag	2159
Db	6369	tttagtggtaaaataatgaagctctccggcccaagccacatagtagaaccttagaagacgag	6428
Oy	2160	actctggagataatcgaatgttgttgttttaagtctgcacgttttgctcacttgta	2219
Db	6429	actctggagataatcgaatgttgttgttttaagtctgcacgttttgctcacttgta	6488
Oy	2220	tgcagcaatagataataataatgcagagaaagag	2253
Db	6489	tgcagcaatagataataataatgcagagaaagag	6522
RESULT 4			
AAZ30053			
AAZ30053 standard; DNA; 7605 BP.			
AAZ30053:			
XX	26-JAN-2000	(first entry)	
XX	DNA encoding a human interleukin-1 receptor antagonist.		
DE	Human; interleukin-1 receptor; IL-1; antagonist; sepsis;		
KW	acute pancreatitis; endotoxin shock; cytokine induced shock;		
KW	rheumatoid arthritis; chronic inflammatory arthritis;		
KW	pancreatic cell damage; diabetes mellitus type 1;		
KW	graft versus host disease; inflammatory bowel disease;		
KW	inflammation; pulmonary disease; autoimmune disease;		
KW	inflammatory disease; antiproliferative; myelogenous leukemia;		
KW	premature labor; intrauterine infection; nutritional activity;		
KW	hematopoiesis regulating activity; tissue growth activity;		
KW	activin activity; inhibin activity; chemotactic activity;		
KW	chemokinetic activity; hemostatic activity; thrombolytic activity;		
KW	anti-inflammatory activity; ss.		
XX	Homo sapiens.		
OS	MO9951744-A2.		
XX	14-OCR-1999.		
XX	05-APR-1999;	99WO-US04291.	
XX	03-APR-1998;	98US-0055010.	
XX	15-MAY-1998;	98US-0079909.	
XX	20-MAY-1998;	98US-0082364.	
XX	19-JUN-1998;	98US-0099818.	
XX	31-JUL-1998;	98US-0127698.	
XX	13-JAN-1999;	99US-0229591.	
XX	17-FEB-1999;	99US-0251370.	
XX	(HYSE-) HYSEQ INC.		
XX	Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;		
XX	Leshkowitz D, Kita D, Ford J, Pace A, Alfentilo M;		
XX	WPI; 1999-611042/52.		
XX	New isolated interleukin-1 receptor binding polypeptides, used to treat		
XX	e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,		
XX	inflammatory disease, autoimmune disease or proliferative disease		
XX	Disclosure; Fig 10A-C; 123pp; English.		
CC	The present sequence encodes a human interleukin-1 (IL-1) receptor		
CC	antagonist. It is an extension of AAZ30052. The encoded polypeptide is		
CC	capable of binding IL-1 receptors (IL-1Rs). The polynucleotides and		

	Query Match	96.8% ; Score 2180.4 ; DB 20 ; Length 7605 ;	
	Best Local Similarity	99.1% ; Pred. No. 0 ;	
	Matches 2234 ;	Conservative 0 ; Mismatches 16 ; Indels 4 ; Gaps 4 ;	
OY	1 aatccaagaattccaccttctacgcgcggagaatgaggctacctccagcttcgagtcgg	60	polypeptides can be used for the prevention or treatment of disorders
Db	5144 aatccaagaattccaccttctacgcgcggagaatgaggctacctccagcttcgagtcgg	5203	CC involving sepsis, acute pancreatitis, endotoxemic shock, cytokine induced
OY	61 ctgcctaccgggctcgttcctcgtgacgctgcgcgaacgcagatccagccgtcaagctca	120	CC Shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic
Db	5204 ctgcctaccgggctcgttcctcgtgacgctgcgcgaacgcagatccagccgtcaagctca	5263	CC cell damage from diabetes mellitus type 1, graft versus host disease,
OY	121 cccagctcccgagaatggttggtcggaaatgcccccatcacagacttctactccagagat	180	CC inflammatory bowel disease, inflammation associated with pulmonary
Db	5264 cccagctcccgagaatggttggtcggaaatgcccccatcacagacttctactccagagat	5323	CC disease, other autoimmune disease or inflammatory disease, an
OY	181 gtgactagggcaacgtgccccccagaaatccctctggagagagccagctcgggtggaggt	240	CC antiproliferative agent such as for acute or chronic myelogenous
Db	5324 gtgactagggcaacgtgccccccagaaatccctctggagagagccagctcgggtggaggt	5382	CC leukemia or in the prevention of premature labor secondary to
OY	241 gagcgagagagaccatctggcgcgaatacatcatctcttctcctccagagcccccagctga	300	CC intratectine infections. They can also exhibit activities such as e.g.
Db	5383 gagcgagagagaccatctggcgcgaatacatcatctctcctcctcgaagcccccaagctga	5442	CC nutritional activity, cytokine and cell proliferation/differentiation
OY	301 cttagcggcacctgacacacttgtctctctgtgtcccaagtttgataaatcttgagatt	360	CC activity, immune stimulating or suppressing activity, hematopoiesis
Db	5443 cttagcggcacctgacacacttgtctctctgtgtcccaagtttgataaatcttgagatt	5502	CC regulating activity, tissue growth activity, activin/inhibin activity,
OY	361 ggaagctaatgccaggtctctcccaacttgagatggtcactgcgtgtgaaaccttgataaa	420	CC chemotactic/ chemokinetic activity, hemostatic and thrombolytic activity,
Db	5503 ggaagctaatgccaggtctctcccaacttgagatggtcactgcgtgtgaaaccttgataaa	5562	CC receptor/ ligand activity, and anti-inflammatory activity. The products
OY	421 accatctgggggtaaacatctgggaataacatgaaaagttctctgtggggctgggtgggggag	480	can also be used for detection, diagnosis and drug screening.
Db	5563 accatctgggggtaaacatctgggaataacatgaaaagttctctgtggggctgggtgggggag	5622	
OY	481 tgcctgggaatcatctcgttacttggttaactgtaacagtgttaacctctgagcccgagacc	540	
Db	5623 tgcctgggaatcatctcgttacttggttaactgtaacagtgttaacctctgagcccgagacc	5682	
OY	541 aaaccatccccaattgagccctataaggttcagctagctctccacatgaaatgcctctcaac	600	
Db	5683 aaaccatccccaattgagccctataaggttcagctagctctccacatgaaatgcctctcaac	5742	
OY	601 accactgtgacagagagaggtgtgtcattatagatctaggagatctatgtgccttggcccaag	660	
Db	5743 accactgtgacagagagaggtgtgtcattatagatctaggagatctatgtgccttggcccaag	5802	
OY	661 cccaccacctctccctt-atccctgcaactgataatgttaccttctctatcctctccctc	719	
Db	5803 cccaccacctctcccttataactctgcaactgtgcaataatgttaaccttctatcctctccctc	5862	
OY	720 atcatctctgtctgtgacatgagaggttggtgattctcagaagaaatggttcgagctcagaa	779	

Dh	5863	atcaatctgtgttgvggcatvgaggaagvtgvtgtaatgctcagaagaatagtcgtgagctcagaa	5922
Qy	780	gataaaagataaavlaagvgtaigtctgaatccctctcttaaaaaaaccagaatatacatcaaaatc	839
Dh	5923	gataaaagataaagtaagvtatgtgtatctctctcttaaaaaaaccagaatatacatcaaaatc	5982
Qy	840	ccagatgctgtctctcatattuccatgaaaagvgctcacaagacatatgtgaaagacctact	899
Dh	5983	ccagatgctgtctctcatattuccatgaaaagvgctcacaagacatatgtgaaagacctact	6042
Qy	900	acaaagvggcatatattgcaaatattcttaattaaagaatacctatttatattcttc	959
Dh	6043	acaaagvggcatatattgcaaatattcttaattaaagaatacctatttatattcttc	6102
Qy	960	ataagaaaaaaagctcvgaaagatttaacttcaattgtatgaatgctcagggvtgtgtgcaat	1019
Dh	6103	ataagaaaaaaagctcvgaaagatttaacttcaattgtatgaatgctcagggvtgtgtgcaat	6162
Qy	1020	agtgatattttctcttcaattctgttaattatctgtatattccctaaattttctacatgaa	1079
Dh	6163	agtgatattttctcttcaattctgttaattatctgtatattccctaaattttctacatgaa	6222
Qy	1080	gataaatctctgtataaaaaataagaagaatataactctgaaagttaagcagagcaagaa	1139
Dh	6223	gataaatctctgtataaaaaataagaagaatataactctgaaagttaagcagagcaagaa	6282
Qy	1140	tcactctctgaatctgctccacagctcccaatctcccaagataaattctcaattgtaatcgagctc	1199
Dh	6283	tcactctctgaatctgctccacagctcccaatctcccaagataaattctcaattgtaatcgagctc	6341
Qy	1200	tgtctgctctgtctgtgtgtatgtatgtatgcagaaacaagatctcagcaaaagccacttga	1259
Dh	6342	tgtctgctctgtctgtgtgtatgtatgtatgcagaaacaagatctcagcaaaagccacttga	6401
Qy	1260	ggaaagcctgctctgaagattgtgtgtgtgcgggaatctctcgggttaagaaacttaaaagaacaaa	1319
Dh	6402	ggaaagcctgctctgaagattgtgtgtgtgcgggaatctctcgggttaagaaacttaaaagaacaaa	6461
Qy	1320	tcactctgttaattctctctctcagaagaagatacaacagccctctgtgaattcacaagagattgtgaatcc	1379
Dh	6462	tcactctgttaattctctctctcagaagaagatacaacagccctctgtgaattcacaagagattgtgaatcc	6521
Qy	1380	agtcctctcaagaagaagctcgtctgactgtgtgaattgtgtgtccctctcaaatctcaatctctct	1439
Dh	6522	agtcctctcaagaagaagctcgtctgactgtgtgaattgtgtgtccctctcaaatctcaatctctct	6581
Qy	1440	tgggaattctcagctctcgtctgaagtttattcttggggataaagttctctcgcacaaatgaatttggttaag	1499
Dh	6582	tgggaattctcagctctcgtctgaagtttattcttggggataaagttctctcgcacaaatgaatttggttaag	6641
Qy	1500	acaaagctcactgctctgagatgaaagvtagaaccccaaaatctcaatatgtactgttctctgtatgaa	1559
Dh	6642	acaaagctcactgctctgagatgaaagvtagaaccccaaaatctcaatatgtactgttctctgtatgaa	6701
Qy	1560	aaggaagagagacacagagacagagagagagacgctcgggtgaagactatgtatgaagaatgaagcagag	1619
Dh	6702	aaggaagagagacacagagacagagagagagacgctcgggtgaagactatgtatgaagaatgaagcagag	6761
Qy	1620	atcggaatttttgcaagccacagaatgaagaacccaagaattgtgtgcaacccatcagaagct	1679
Dh	6762	atcggaatttttgcaagccacagaatgaagaacccaagaattgtgtgcaacccatcagaagct	6821
Qy	1680	tgggaagagagacaaagaagaattctctccctcagagctttaaaggtataaagcctcgtcgaa	1739
Dh	6822	tgggaagagagacaaagaagaattctctccctcagagctttaaaggtataaagcctcgtcgaa	6881
Qy	1740	accttaattctcagaattctcagacctctctgtgaacgaagaagaataaattctcggctgttttaa	1799
Dh	6882	accttaattctcagaattctcagacctctctgtgaacgaagaagaataaattctcggctgttttaa	6941
Qy	1800	ggcaaccaagataattgtgttaacgcaagctctctggaacccaataacagctcgtcacaagtatgc	1859
Dh	6942	ggcaaccaagataattgtgtgtatgtggcagctctctggaacccaataacagctcgtcacaagtatgc	7001

QY	1860	ccgtgtccctcgtgtgttacaattcctggtgtgtgtccctccccaacaaatgtaccaaaagtgtct	191
Db	7002	ccgtgtccctcgtgtgttacaattcctggtgtgtgtccctccccaacaaatgtaccaaaagtgtct	706
QY	1920	ttgtgaccacaaatagaataatgcagcaagtgatgtgcattgcacatcccaagattaaagtataa	197
Db	7062	ttgtgta-ccaaatagaataatgcagcaagtgatgtgcattgcacatcccaagattaaagtataa	712
QY	1960	aagacatctgcagcttctaacttgaagccctctctctctgcacacacgcgcgcacacatctac	203
Db	7121	aagacatctgcagcttctaacttgaagccctctctctctgcacacacgcgcgcacacatctac	718
QY	2040	ttgtgtcaatctgcctctgcgggaagctgagccatgtatgaacagagccatataaagagc	209
Db	7181	ttgtgtcaatctgcctctgcgggaagctgagccatgtatgaacagagccatataaagagac	724
QY	2100	ttacgtgttaaaaaatgaagctctctctcccaacagccacatgaatgaacctagaagcagag	215
Db	7241	ttatgtgttaaaaaatgaagctctctctcccaacagccacatgaatgaacctagaagcagag	730
QY	2160	actctgtgagataatcgaatgtttgtgtttttaaagttgcacgttttggctaaactgtta	221
Db	7301	actctgtgagataatcgaatgtttgtgtttttaaagttgcacgttttggctaaactgtta	736
QY	2220	tgcagcaatagataataataatgtgaaggaagag	2253
Db	7361	tgcagcaatagataataataatgtgaaggaagag	7394
RESULT 5			
AAEF31356			
ID	AAEF31356 standard; DNA; 7605 BP.		
XX			
AC	AAEF31356:		
XX			
DT	05-APR-2001 (first entry)		
XX			
DE	Extension of genomic clone B2HPLS20W.		
XX			
KW	Interleukin; IL-1 receptor; cancer; inflammation; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200102571-A2.		
XX			
PD	11-JAN-2001.		
XX			
PF	07-JUL-2000; 2000WO-US18710.		
XX			
PR	07-JUL-1999; 99US-0348942.		
PR	13-OCT-1999; 99US-0417455.		
PR	08-DEC-1999; 99US-0457626.		
PR	10-MAR-2000; 2000US-0523552.		
PR	22-MAY-2000; 2000US-0576008.		
XX			
PA	(HYSEQ-) HYSEQ INC.		
XX			
PI	Ford J. Pace A:		
DR	WPI: 2001-071582/08.		
XX			
PT	Isolated nucleic acids encoding interleukin-1 (IL-1) receptor		
PT	antagonist proteins (referred as IL-1HY1), useful in the treatment of		
PT	cancer, e.g. breast adenocarcinoma and brain tumors, and an		
PT	inflammatory disease mediated by IL-18 -		
XX			
PS	Disclosure: Fig 10; 179pp; English.		
XX			
CC	The present invention relates to interleukin (IL)-1 receptor		
CC	antagonist proteins. IL-1HY1 is useful for treating cancer,		
CC	an inflammatory disease mediated by IL-18, inflammation		
CC	resulting from infection or allergic reactions, and inflammation		

CC The present invention relates to interleukin (IL)-1 receptor  
CC antagonist proteins. IL-1H1 is useful for treating cancer,  
CC an inflammatory disease mediated by IL-18, inflammation  
CC resulting from infection or allergic reactions, and inflammation

CC associated with chronic bronchitis, arthritis, diabetes or  
CC endothermia.

XX Sequence 7605 BP; 2079 A; 1647 C; 1865 G; 2009 T; 5 other;

Query Match 96.8%; Score 2180.4; DB 22; Length 7605;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2234; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

QY 1 aatccaagagcttccattctacacgaggaatgaggtacacccagcttgagtcgg 60  
DB 5144 aatccaagagcttccattctacacgaggaatgaggtacacccagcttgagtcgg 5203  
QY ctgcctaccggcggtggtctctgctgcaacggtgctcgaagccatcagctctcagactca 120  
DB 5204 ctgcctaccggcggtggtctctgctgcaacggtgctcgaagccatcagctctcagactca 5263  
QY 121 cccagcttcccgagaaatggtggtggaatgccccatcacagacttctactccagcagt 180  
DB 5264 cccagcttcccgagaaatggtggtggaatgccccatcacagacttctactccagcagt 5323  
QY 181 gtagactaggagcaagctgccccccagaaactccctggcagagccagctcgggtgaggggt 240  
DB 5324 gtagactaggagcaagctgccccccagaaactccctggcagagccagctcgggtgaggggt 5382  
QY 241 gagtggagagagacccaatgagcagacaatcactctctctgctctcagagcccccaggtctga 300  
DB 5383 gagtggagagagacccaatgagcagacaatcactctctctgctctcagagcccccaggtctga 5442  
QY 301 cttagtgaggacacctgacacttctctctggttccaggttcgataaatctcagatctt 360  
DB 5443 cttagtgaggacacctgacacttctctctggttccaggttcgataaatctcagatctt 5502  
QY 361 ggaagctcagatccagaggtccctcccaactggatggtgctacagctctggaacctgtgataaa 420  
DB 5503 ggaagctcagatccagaggtccctcccaactggatggtgctacagctctggaacctgtgataaa 5562  
QY 421 accatgtgaggtaaacctgggaaataacatgtaaaagaattctgttgagggtgagggtggaggag 480  
DB 5563 accatgtgaggtaaacctgggaaataacatgtaaaagaattctgttgagggtgagggtggaggag 5622  
QY 481 tgcctgggaatcatctctctgttaaatgttaactggaacagtgtaaccttgagcccgcaagcc 540  
DB 5623 tgcctgggaatcatctctctgttaaatgttaactggaacagtgtaaccttgagcccgcaagcc 5682  
QY 541 aacccatcccccaggttgagcctataggttcagtaagctctccacatgaaagtctctgtaactc 600  
DB 5683 aacccatcccccaggttgagcctataggttcagtaagctctccacatgaaagtctctgtaactc 5742  
QY 601 accactgtgagagagagagggtggtcatalagatcagagatctatgaccttgagccagc 660  
DB 5743 accactgtgagagagagagggtggtcatalagatcagagatctatgaccttgagccagc 5802  
QY 661 cccacccccccttccctt-attcctgactgtgatagttactcttccatcttccctc 719  
DB 5803 cccacccccccttccctt-attcctgactgtgatagttactcttccatcttccctc 5862  
QY 720 atcatctctgttgagcagtaagaggtgtgagtgatcagaagaatgtgtcagctcagaa 779  
DB 5863 atcatctctgttgagcagtaagaggtgtgagtgatcagaagaatgtgtcagctcagaa 5922  
QY 780 gataaaagaataagtaggtatgctgtaaccctctttaaaccacccaagatatacaataatc 839  
DB 5923 gataaaagaataagtaggtatgctgtaaccctctttaaaccacccaagatatacaataatc 5982  
QY 840 ccaagatgctggtctctatctcccatgaaaaagtgtccatgacatatgtgagaagactactc 899  
DB 5983 ccaagatgctggtctctatctcccatgaaaaagtgtccatgacatatgtgagaagactactc 6042  
QY 900 acaaagtgcacatatgtcaaatcttaatttaaatgaaagatccatataatcttctt 959  
DB 6043 acaaagtgcacatatgtcaaatcttaatttaaatgaaagatccatataatcttctt 6102

QY 960 atagaaaaaagctctgaaagatttacttcaattgtgaaatgtcagggtggtgagcagctat 1019  
DB 6103 atagaaaaaagctctgaaagatttacttcaattgtgaaatgtcagggtggtgagcagctat 6162  
QY 1020 aggtgatttcttcttaattcgttaatttactgtaattcttcaatttctctacaatgaa 1079  
DB 6163 aggtgatttcttcttaattcgttaatttactgtaattcttcaatttctctacaatgaa 6222  
QY 1080 gatgaaattcctgtataaaaaataaagaagaataattcgtgaagtgaagagcgagaca 1139  
DB 6223 gatgaaattcctgtataaaaaataaagaagaataattcgtgaagtgaagagcgagaca 6282  
QY 1140 tcatctctgattctcctcagccctcccaattcccgaggttaaatctcaaatctgaatcagctc 1199  
DB 6283 tcatctctgattctg-ctcctagcctccacttcccgaggttaaatctcaaatctgaatcagctc 6341  
QY 1200 tgcctgctctgttgggttgtagtagtgcataaggaacagatctcagcaaacctgagga 1259  
DB 6342 tgcctgctctgttgggttgtagtagtgcataaggaacagatctcagcaaacctgagga 6401  
QY 1260 ggaagctggtcaggttgggtggtggaatctctggttaaggaacttaagaacaaa 1319  
DB 6402 ggaagctggtcaggttgggtggtggaatctctggttaaggaacttaagaacaaa 6461  
QY 1320 tcatctgtaattcttctcctagaagaagatcacagcccttgaggtatcccaaggtatgattcc 1379  
DB 6462 tcatctgtaattcttctcctagaagaagatcacagcccttgaggtatcccaaggtatgattcc 6521  
QY 1380 agtctctaagaagctctgctgtacgtgttgaattgtgttccctcaaatctcaatctctct 1439  
DB 6522 agtctctaagaagctctgctgtacgtgttgaattgtgttccctcaaatctcaatctctct 6581  
QY 1440 tgaatctcagctctgtgagttatttggagaataaggtctctgcagatgtagttagtaag 1499  
DB 6582 tgaatctcagctctgtgagttatttggagaataaggtctctgcagatgtagttagtaag 6641  
QY 1500 acaaggtcagctctgagtgaaagtgagccataaattcaatgatctgttctctgtatgaa 1559  
DB 6642 acaaggtcagctctgagtgaaagtgagccataaattcaatgatctgttctctgtatgaa 6701  
QY 1560 aaggaagagacacaaagacagagagagacgaggaagacatctgtaaaagaatgaagcgag 1619  
DB 6702 aaggaagagacacaaagacagagagagacgaggaagacatctgtaaaagaatgaagcgag 6761  
QY 1620 atcggagtttctcagcccaagcttaagaagaacacaaagatgtgtgcacaacatcagaagct 1679  
DB 6762 atcggagtttctcagcccaagcttaagaagaacacaaagatgtgtgcacaacatcagaagct 6821  
QY 1680 tggaaagagcacaagaagaattcttccctagaagctttagaggataacggtctgtgaa 1739  
DB 6822 tggaaagagcacaagaagaattcttccctagaagctttagaggataacggtctgtgaa 6881  
QY 1740 accttaattctgaagcttccagctctctgaaagaaagaataaatttggcgtgttttaa 1799  
DB 6882 accttaattctgaagcttccagctctctgaaagaaagaataaatttggcgtgttttaa 6941  
QY 1800 gccaccaagataatctgttacaagagctctcaggaacataatacagctgtctaaatgatac 1859  
DB 6942 gccaccaagataatctgttacaagagctctcaggaacataatacagctgtctaaatgatac 7001  
QY 1860 cctgtctccctgttcttaacattctgtgtgttccctcccaaatgttaacaaagtgtctc 1919  
DB 7002 cctgtctccctgttcttaacattctgtgtgttccctcccaaatgttaacaaagtgtctc 7061  
QY 1920 ttgtgacccaatagaataatgtgcagaagatgagatgacattccattcaagattaggtttata 1979  
DB 7062 ttgtgacccaatagaataatgtgcagaagatgagatgacattccattcaagattaggtttata 7120  
QY 1980 aagacaatgcagctctacttgaagccctctctctgcccacacacgccccacatctac 2039  
DB 7121 aagacaatgcagctctacttgaagccctctctctctgcccacacacgccccacatctac 7180



QY 2040 ttggtcactcgtctcgtgggaagctagctcgtcgtatagcaagcctataaagac 2099  
|||||  
Db 7181 ttggtcactcgtctcgtgggaagctagctcgtcgtatagcaagcctataaagac 7240  
QY 2100 ttacgttgtaaaaaatgaagctctctccacacagccacatlagtgaacctagaagcagag 2159  
|||||  
Db 7241 ttatggttaaaaaatgaagctctctccacacagccacatlagtgaacctagaagcagag 7300  
QY 2160 acctgttgagataatcgtatgttctgttttaagtgtcgtcagtttctgttaactgtta 2219  
|||||  
Db 7301 acctgttgagataatcgtatgttctgttttaagtgtcgtcagtttctgttaactgtta 7360  
QY 2220 tgcagcaatagataataatcatgcagagaagaag 2253  
|||||  
Db 7361 tgcagcaatagataataatcatgcagagaagaag 7394

RESULT 6  
1354  
AAF31354 standard: cDNA; 2647 BP.

AC AAF31354;  
XX  
DT 05-APR-2001 (first entry)  
XX  
DE Extension of B2HFLS20W cDNA library sequence #2.  
XX  
KM Interleukin: IL-1 receptor; cancer: Inflammation; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200102571-A2.  
XX  
PD 11-JAN-2001.  
XX  
PF 07-JUL-2000; 2000MO-US18710.  
XX  
PR 07-JUL-1999; 99US-0348942.  
PR 13-OCT-1999; 99US-0417455.  
PR 08-DEC-1999; 99US-0457626.  
PR 10-MAR-2000; 2000US-0523552.  
PR 22-MAY-2000; 2000US-0576008.  
XX  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Ford J, Pace A;  
WPI; 2001-071582/08.

PT Isolated nucleic acids encoding Interleukin-1 (IL-1) receptor  
PT antagonist proteins (referred as IL-1hY1), useful in the treatment of  
PT cancer, e.g. breast adenocarcinoma and brain tumors, and an  
PT inflammatory disease mediated by IL-18 -  
XX  
XX  
PS Claim 1; Fig 8; 179pp; English.  
XX  
XX  
CC The present invention relates to interleukin (IL)-1 receptor  
CC antagonist proteins. IL-1hY1 is useful for treating cancer,  
CC an inflammatory disease mediated by IL-18, inflammation  
CC resulting from infection or allergic reactions, and inflammation  
CC associated with chronic bronchitis, arthritis, diabetes or  
CC endohermia.  
XX  
XX  
SQ Sequence 2647 BP; 743 A; 589 C; 644 G; 671 T; 0 other;

Query Match 96.7%; Score 2178.4; DB 22; Length 2647;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2240; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

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Db 462 ccagacttcccggaatctgtgtctggaatgcccccatcaagacttctacttccagcagt 521  
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QY 421 accatgtgggttaaacctgggaataacatgaagaagattctcgtgggggtgggggtggag 480  
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 QY 1739 aaccttaattcagactcagactcagcctcctcgaacgaagaagaataatttcgctgttcta 1798  
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 Db 2081 aaccttaattcagactcagactcagcctcctcgaacgaagaagaataatttcgctgttcta 2140  
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 QY 1799 agccaccaagataatttggttaccagagctcctaggaacataaatacagctgtctaaatgat 1858  
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 QY 1859 cccgtctctcgtgttataatctgtgtgtgtccctcccaacatgataccaaagtgtc 1918  
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 Db 2201 cccgtctctcgtgttataatctgtgtgtgtccctcccaacatgataccaaagtgtc 2260  
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 |||  
 Db 2261 ttgtgacccaatagaaatagatgagcagatgtagtgcactctccaagattagttata 2319  
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 QY 2099 cttaagctggttaaaaaatgaagctctctgcccacagccacattagtgaaacttagaagcaga 2158  
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 Db 2440 cttaagctggttaaaaaatgaagctctctgcccacagccacattagtgaaacttagaagcaga 2499  
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Db 2560 tatgacgaataagataataataatagcagagaagaag 2595  
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 RESULT 7  
 AAZ30051  
 ID AAZ30051 standard; CDNA: 2648 BP.  
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 AC AAZ30051;  
 XX  
 DT 26-JAN-2000 (first entry)  
 XX  
 DE CDNA encoding a human interleukin-1 receptor antagonist.  
 XX  
 KW Human; interleukin-1 receptor; IL-1; antagonist; sepsis;  
 KW acute pancreatitis; endotoxic shock; cytokine induced shock;  
 KW rheumatoid arthritis; chronic inflammatory arthritis;  
 KW pancreatic cell damage; diabetes mellitus type 1;  
 KW graft versus host disease; inflammatory bowel disease;  
 KW inflammation; pulmonary disease; autoimmune disease;  
 KW inflammatory disease; antiproliferative; myelogenous leukemia;  
 KW premature labor; intrauterine infection; nutritional activity;  
 KW hematopoiesis regulating activity; tissue growth activity;  
 KW activin activity; inhibin activity; chemotactic activity;  
 KW chemokine activity; hemostatic activity; thrombolytic activity;  
 KW anti-inflammatory activity; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9951744-A2.  
 XX  
 PD 14-OCT-1999.  
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 PF 05-APR-1999; 99WO-US04291.  
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 PR 03-APR-1998; 98US-0055010.  
 PR 15-MAY-1998; 98US-0079909.  
 PR 20-MAY-1998; 98US-0082364.  
 PR 19-JUN-1998; 98US-0099818.  
 PR 31-JUL-1998; 98US-0127698.  
 PR 13-JAN-1999; 99US-0229591.  
 PR 17-FEB-1999; 99US-0251370.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Drmanac R, Crikvenjakov R, Dickson M, Drmanac S, Labat I;  
 PI Leshkowitz D, Kila D, Ford J, Pace A, Alfento M;  
 PI  
 XX  
 DR WPI: 1999-611042/52.  
 XX  
 PT New isolated interleukin-1 receptor binding polypeptides, used to treat  
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,  
 PT inflammatory disease, autoimmune disease or proliferative disease -  
 XX  
 PS Claim 1, Fig 8: 123pp: English.  
 XX  
 CC The present sequence encodes a human interleukin-1 (IL-1) receptor  
 CC antagonist. It is an extension of AAZ30050. The encoded polypeptide is  
 CC capable of binding IL-1 receptors (IL-1Rs). The polynucleotides and  
 CC polypeptides can be used for the prevention or treatment of disorders  
 CC involving sepsis, acute pancreatitis, endotoxic shock, cytokine induced  
 CC shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic  
 CC cell damage from diabetes mellitus type 1, graft versus host disease,  
 CC inflammatory bowel disease, inflammation associated with pulmonary  
 CC disease, other autoimmune disease or inflammatory disease, an  
 CC antiproliferative agent such as for acute or chronic myelogenous  
 CC leukemia or in the prevention of premature labor secondary to  
 CC intrauterine infections. They can also exhibit activities such as e.g.  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating or suppressing activity, hematopoiesis  
 CC regulating activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokine activity, hemostatic and thrombolytic activity,  
 CC receptor/ligand activity, and anti-inflammatory activity. The products

CC can also be used for detection, diagnosis and drug screening.  
XX  
Sequence 2648 BP; 744 A; 589 C; 644 G; 671 T; 0 other;

Query Match		96.7%;	Score 2178.4;	DB 20;	Length 2648;
Best Local Similarity		99.3%;	Pred. No. 0;		
Matches 2240; Conservative		0;	Mismatches 11;	Indels 5;	Gaps 5;
QY	1	aatccaagagcttcaacattccacgcygagacatgggtctcaactccagcttcgagtcg	60		
DB	342	aatccaagagcttcaacattccacgcygagacatgggtctcaactccagcttcgagtcg	401		
QY	61	cgcgcacacgggctggtctcctctgacagcgctccctgaagcccatcagctctgacatca	120		
DB	402	cgcgcacacgggctggtctcctctgacagcgctccctgaagcccatcagctctgacatca	461		
QY	121	cccagcttcccgagaaatggctggtgaatgcccccatcacaagacttacttccagcagt	180		
DB	462	cccagcttcccgagaaatggctggtgaatgcccccatcacaagacttacttccagcagt	521		
QY	181	gtgactagggcaacgtgcccccccaaacctccctgggcagagccagctcgggtgaggg	240		
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DB	581	gggtgagagagaccacatggcgcgacaaatcaactctctctctcagagaccgggtctga	640		
QY	301	cttaagtgggacacctgacacacttgtctctggttcccaagtcttgacataaattctgaatlt	360		
DB	641	cttaagtgggacacctgacacacttgtctctggttcccaagtcttgacataaattctgaatlt	700		
QY	361	ggaagctcaatccaaggtccctcccccacatgagtgctactctgtctggaaccttgtaaa	420		
DB	701	ggaagctcaatccaaggtccctcccccacatgagtgctactctgtctggaaccttgtaaa	760		
QY	421	accagtctgggctaaacttgggaataacatgaagaattctctgggggttgggtgggggag	480		
DB	761	accagtctgggctaaacttgggaataacatgaagaattctctgggggttgggtgggggag	820		
QY	481	tgctgggaatcatctcgtcttaattggtaactgacaagtgttacccttgagcccgagcgc	540		
DB	821	tgctgggaatcatctcgtcttaattggtaactgacaagtgttacccttgagcccgagcgc	880		
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DB	1061	atcatctctgttgggcaatgagggaggtgtgtatgtcagaagaatgtgtccgagctcaga	1120		
QY	780	gataaagaataagtagtagtctgactcctctttaaataaaccataatcaatacaaatc	839		
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QY	840	ccagatgtcgtctctatcccatcgaataaagtgtcatalgacatlatggaagaaccactt	899		
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QY	959	tatagaataaagctctggaagagcttactcaattctgtagcaatgcatggctggtgagta	1018		
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QY	1679	ctggaagagcacaagaagaatcttccctagaaggtcttgaagagatcaacgctctgtga	1738		
DB	2021	ctggaagagcacaagaagaatcttccctagaaggtcttgaagagatcaacgctctgtga	2080		
QY	1739	aaccttaatctcagacttccagcctctcgaacgaagaagaataaattccgctgttca	1798		
DB	2081	aaccttaatctcagacttccagcctctcgaacgaagaagaataaattccgctgttca	2140		
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DB	2261	tttgtgacccaatagaataatggcagaagtgtatgcatctgcaacttccaagattaggttata	2319		
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Qy 2159 gactcgtgagataacacgattgttctgtctt-aagttgctcagttctgtcctaactgt 2217
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RESULT 8
AAZ50813
ID AAZ50813 standard; cDNA; 2490 BP.
XX
AC AAZ50813;
31-MAY-2000 (first entry)

Human TANGO-93 cDNA with additional 3'UTR sequence.
DE
XX TANGO-93; cytokine; human; secreted protein; IL-1 expression; cancer;
XX Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
XX immunosuppressive; antihemematic; antiarthritic; antipsoriatic; asthma;
XX antiinflammatory; antibacterial; antitumor; cytosstatic; immunomodulator;
XX osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
XX graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;
XX septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;
XX liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
XX autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
XX systemic lupus erythematosus; forensic; transgenic animal; SS.
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XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX /note= "Has 53% homology to human Interleukin-1 receptor
XX 3'UTR 531..2490
XX /tag= b
XX /note= "Additional sequences"

XX MO200008045-A2.
XX
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99MO-US17886.
XX
XX 07-AUG-1998; 98US-0131263.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Pan Y;
XX
XX WPI; 2000-205669/18.
XX
XX Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful
XX for treating a variety of cellular processes e.g. asthma, rheumatoid
XX arthritis, psoriasis and autoimmune diseases
XX
XX Example 2; Fig 5; 113pp; English.
XX
XX The present sequence is the cDNA encoding the human TANGO-93, with
XX additional 3'UTR sequence. It is a secreted protein that belongs to the
XX cytokine superfamily. It plays a role similar to secreted interleukin-1
XX receptor antagonist (IL-1ra). TANGO-93 modulates immune mediated
```

```
CC inflammation and IL-1 gene or protein expression. TANGO-93 is useful as
CC a modulating agent for regulating cellular processes like asthma, graft
CC vs-host disease, rheumatoid arthritis, psoriasis, inflammatory bowel
CC disease, septic shock, ulcerative colitis, Crohn's disease, chronic
CC myelogenous leukemia, cancer, liver disease, Hodgkin's disease,
CC osteoarthritis, Lyme disease, cachexia, and autoimmune diseases e.g.
CC myasthenia gravis, autoimmune diabetes and systemic lupus erythematosus.
CC Partial TANGO-93 sequences are useful in forensic biology, for diagnostic
CC and prognostic assays, prophylactic and therapeutic treatment and
CC pharmacogenomics. The DNA sequences are useful as hybridization probes
CC and primers, for isolation of TANGO-93 sequence and for the creation of
CC transgenic animals.
XX
XX Sequence 2490 BP; 650 A; 571 C; 619 G; 650 T; 0 other;
XX
XX
XX Query Match 89.7%; Score 2020.6; DB 21; Length 2490;
XX Best Local Similarity 96.3%; Pred. No. 0;
XX Matches 2138; Conservative 0; Mismatches 9; Indels 72; Gaps 4;
Qy 1 aatcagaagcttcaaccttctacccggcggaatgaggctaacctcagctcagtcg 60
Db 343 aatcagaagcttcaaccttctacccggcggaatgaggctaacctcagctcagtcg 402
Qy 61 ctgctaccgggctggtctcctgacagtgctgaaagccgatcagctcagactca 120
Db 403 ctgctaccgggctggtctcctgacagtgctgaaagccgatcagctcagactca 462
Qy 121 ccagcttccgaagatggtgctggaatgcccatacagacttactcagcagat 180
Db 463 ccagcttccgaagatggtgctggaatgcccatacagacttactcagcagat 522
Qy 181 gtacacaggcgaacgtgccccccagaactcccttgggagagcagctcgggtgag 240
Db 523 gtacacaggcgaacgtgccccccagaactcccttgggagagcagctcgggtgag 581
Qy 241 gaatgagagagaccatgagggaacaatcactcttctgcttcagagaccagctga 300
Db 582 gaatgagagagaccatgagggaacaatcactcttctgcttcagagaccagctga 641
Qy 301 cttaggggacacgtacacacttctctctgcttccaggttgatataatctgagatt 360
Db 642 cttaggggacacgtacacacttctctctgcttccaggttgatataatctgagatt 701
Qy 361 ggaagcgaatccagggtccctccccaactgagatgctcactgctgtaaacctgtaaa 420
Db 702 ggaagcgaatccagggtccctccccaactgagatgctcactgctgtaaacctgtaaa 761
Qy 421 accatgtgggttaaacctgggaataacatgaaagaattctgtgggggtggggag 480
Db 762 accatgtgggttaaacctgggaataacatgaaagaattctgtgggggtggggag 821
Qy 481 tgcctggaatcattcctgttaagtgaactgacaagtgctacccctagccccagagcc 540
Db 822 tgcctggaatcattcctgttaagtgaactgacaagtgctacccctagccccagagcc 881
Qy 541 aaccacatcccaactgtagcctataaggttcagtgacttcacatgaaagtcctcactc 600
Db 882 aaccacatcccaactgtagcctataaggttcagtgacttcacatgaaagtcctcactc 941
Qy 601 accacgtgcaagagagaggtggtcatatagatcaggaactatgaccttgccagc 660
Db 942 accacgtgcaagagagaggtggtcatatagatcaggaactatgaccttgccagc 1001
Qy 661 cccaccccttcctt-ctcctgcaactgataatgctacttctcattctccctc 719
Db 1002 cccaccccttcctt-ctcctgcaactgataatgctacttctcattctccctc 1061
Qy 720 atcatctgttgaggcaagagaggtggtcatgcaagaagaatggttcgagctcagaa 779
Db 1062 atcatctgttgaggcaagagaggtggtcatgcaagaagaatggttcgagctcagaa 1121
Qy 780 gataaagaatagtaggtatgctatcctctttaaataaccacaagatacataaatac 839
```



oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AA829446 to AA859593 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

**SQ** Sequence 1866 BP; 539 A; 383 C; 429 G; 515 T; 0 other;

Query Match	81.4%	Score 1835;	DB 22;	Length 1866;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1860; Conservative	0;	Mismatches 5;	Indels 2;	Gaps 2;

00	386	actgtagtgctcctcctcttggaacctgttaaaacccatgtggggtaaacgvggaaataa	445
01	1	actgtagtgctcctcctcttggaacctgttaaaacccatgtggggtaaacgvggaaataa	60
	446	catgaaagaatctctgtggygggtcgtggggtcgtgggagtgtcgtgggaatcatctcgtctaagt	505
02	61	catgaaagaatctctcgtggygggtcgtggggtcgtgggagtgtcgtgggaatcatctcgtctaagt	120
03	506	gtaaactgacaagtggtttaccccttgagcccgagagccaaaccatccccaagtctgagccttaata	565
04	121	gtaaactgacaagtggtttaccccttgagcccgagagccaaaccatccccaagtctgagccttaata	180
05	566	gggtcgaatgagctctccacatcgtgaagctccctccacatccacacgtctgcagaggaagggagtggtg	625
06	181	gggtcgaatgagctctccacatcgtgaagctccctccacatccacacgtctgcagaggaagggagtggtg	240
07	626	tcatagagtcagaggatctaatgtgcctctgtgcccagccagcccaaccctctccctt-atcctgc	684
08	241	tcatagagtcagaggatctaatgtgcctctgtgcccagccagcccaaccctctccctt-atcctgc	300
09	685	cacgtcctaatagcctacacctttccatctcctccatccatctgtgtgtgtggtggatagaagag	744
10	301	cacgtcctaatagcctacacctttccatctcctccatccatctgtgtgtgtggtggatagaagag	360
11	745	gtggtagtgtcagaagaagaatctgtgtcagctccacaagaataaaagaataagtagagtagtctgtg	804
12	361	gtggtagtgtcagaagaagaatctgtgtcagctccacaagaataaaagaataagtagagtagtctgtg	420
13	805	atcctctctttaaaaaaccacaagatacaataatccacagatgcgtgtctctatctcccatg	864
14	421	atcctctctttaaaaaaccacaagatacaataatccacagatgcgtgtctctatctcccatg	480
	865	aaaaagtgctcatgacatatcttgagaagacctactttacaagtggtcatatatctgcaattta	924
15	481	aaaaagtgctcatgacatatcttgagaagacctactttacaagtggtcatatatctgcaattta	540
16	925	tcttaatataaagaatacctaattatattctcttaagaaaaaagctcggaagagttta	984
17	541	tcttaatataaagaatacctaattatattctcttaagaaaaaagctcggaagagttta	600
18	985	cttcaatctgtagcaatgtcagagggtgtgtagcagtagatggtatcttctttaatcttgt	1044
19	601	cttcaatctgtagcaatgtcagagggtgtgtagcagtagatggtatcttctttaatcttgt	660
20	1045	aattatctgtatctcctaattttctctacaagaagaatgaattctccttgtataaaaataag	1104
21	661	aattatctgtatctcctaattttctctacaagaagaatgaattctccttgtataaaaataag	720
22	1105	aaaagaataatcaattcttaggtagaacagagagaacatcagatctcgtatgtccccaagccccc	1164
23	721	aaaagaataatcaattcttaggtagaacagagagaacatcagatctcgtatgtccccaagccccc	780
24	1165	aattccccaagataatctcaaatctgaatcagagctctgcgtcctcgtgtgtgtgtgtgtgtgt	1224

Db 1860 gagaag 1866

RESULT 10  
AAF31355  
ID AAF31355 standard; DNA: 5751 BP.  
XX  
AC AAF31355;  
XX  
DT 05-APR-2001 (first entry)  
XX  
DE Genomic clone B2HFLS20W.  
XX  
KW Interleukin; IL-1 receptor; cancer; inflammation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200102571-A2.  
XX  
11-JAN-2001.  
XX  
PF 07-JUL-2000; 2000WO-US18710.  
XX  
PR 07-JUL-1999; 99US-0348942.  
PR 13-OCT-1999; 99US-0417455.  
PR 08-DEC-1999; 99US-0457626.  
PR 10-MAR-2000; 2000US-0523552.  
PR 22-MAY-2000; 2000US-0576008.  
XX  
PA (HYSE-) HXSEQ INC.  
XX  
PI Ford J, Pace A;  
XX  
DR WPI: 2001-071582/08.  
XX  
XX  
PT Isolated nucleic acids encoding Interleukin-1 (IL-1) receptor  
PT antagonist proteins (referred as IL-1H1), useful in the treatment of  
PT cancer, e.g. breast adenocarcinoma and brain tumors, and an  
PT inflammatory disease mediated by IL-18 -  
XX  
PS Claim 1: Fig 9; 179pp: English.  
XX  
XX  
CC The present invention relates to Interleukin (IL)-1 receptor  
CC antagonist proteins. IL-1H1 is useful for treating cancer,  
CC an inflammatory disease mediated by IL-18, inflammation  
CC resulting from infection or allergic reactions, and inflammation  
CC associated with chronic bronchitis, arthritis, diabetes or  
CC endothermia.  
SQ Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 139 other:

Query Match 70.0%; Score 1577.6; DB 22; Length 5751;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1624; Conservative 5; Mismatches 9; Indels 4; Gaps 4;

QY 1 aatcaagaagcttcaactctacacggcgagacatggggtctcaactccagcttcagtcg 60  
Db 4112 aatcaagaagcttcaactctacacggcgagacatggggtctcaactccagcttcagtcg 4171

QY 61 cgcgctacccggcgctggtctcgtgcaacgtgctgaagccgacatcagctgtcagatca 120  
Db 4172 cgcgctacccggcgctggtctcgtgcaacgtgctgaagccgacatcagctgtcagatca 4231

QY 121 ccagagctccgagaaatggtgagatgagccccaatcacaagactctactctccagagat 180  
Db 4232 ccagagctccgagaaatggtgagatgagccccaatcacaagactctactctccagagat 4291

QY 181 gtcgactaaggagcaagtcgccccccaagaactccttgagcagaagccaactggtgagaggt 240  
Db 4292 gtcgactaaggagcaagtcgccccccaagaactccttgagcagaagccaactggtgagaggt 4350

QY 241 gagtgagagagaccatggcgagacaatcactcttctgctcagagaccacaggtctga 300

Db 4351 gagtgagagagaccatggcgagacaatcactcttctgctcagagaccacaggtctga 4410

QY 301 cttagtgagacactgacacacttctctctggtctccagttgcataaattctgagattc 360  
Db 4411 cttagtgagacactgacacacttctctctggtctccagttgcataaattctgagattc 4470

QY 361 ggaagctcagatccagggtctcccccagatgagtgctactctgtctggaactcttaaa 420  
Db 4471 ggaagctcagatccagggtctcccccagatgagtgctactctgtctggaactcttaaa 4530

QY 421 accatgtgaggtaaaactgagaaataacatgaagaattctctgagggtgagggtgagg 480  
Db 4531 accatgtgagggtaaactgagaaataacatgaagaattctctgagggtgagggtgagg 4590

QY 481 tgcctgggaatcattccctgtctaaatggttaactgacaaatggttaacctgagccgagcc 540  
Db 4591 tgcctgggaatcattccctgtctaaatggttaactgacaaatggttaacctgagccgagcc 4650

QY 541 aaccatcccccagttgagcttataggtcagtgagctctccacatgaaatctctcactc 600  
Db 4651 aaccatcccccagttgagcttataggtcagtgagctctccacatgaaatctctcactc 4710

QY 601 accactgtgagagagagaggtggtcatalagatcagagatcattgagcccttgagccagc 660  
Db 4711 accactgtgagagagagaggtggtcatalagatcagagatcattgagcccttgagccagc 4770

QY 661 cccaccccccctccctt-atcctgcacatgcatatgcttaaccttctctctctcctc 719  
Db 4771 cccaccccccctccctt-atcctgcacatgcatatgcttaaccttctctctctcctcctc 4830

QY 720 atcatctgtgtggtgagagaggtggtggtatgcatgaagaagaatggtctcaggtccaga 779  
Db 4831 atcatctgtgtggtgagagaggtggtggtatgcatgaagaagaatggtctcaggtccaga 4890

QY 780 gataaagaataagtgaggtatgctgatactcctctttaaaccacaaatgataatcaaaat 838  
Db 4891 gataaagaataagtgaggtatgctgatactcctctttaaaccacaaatgataatcaaaat 4950

QY 839 cccagatgctgtctctctatcccatgaaanaatgctccatgacatatttggaagacctact 898  
Db 4951 cccagatgctgtctctctatcccatgaaanaatgctccatgacatatttggaagacctact 5010

QY 899 tacaagtgagcatatattcaatttatttaattaaagaatccattatattctt 958  
Db 5011 tacaagtgagcatatattcaatttatttaattaaagaatccattatattctt 5070

QY 959 tatagaaaaaagcttgaagaagttactcaattgtagcaatgctcaggttggctgagatga 1018  
Db 5071 tatagaaaaaagcttgaagaagttactcaattgtagcaatgctcaggttggctgagatga 5130

QY 1019 tagtgatcttctctttaaattctgttaatttactgtatcttccctaatttcttacaatga 1078  
Db 5131 tagtgatcttctctttaaattctgttaatttactgtatcttccctaatttcttacaatga 5190

QY 1079 agatgaatcctgtataaanaataagaagaatattcaattctgaggtgaagcagagcagc 1138  
Db 5191 agatgaatcctgtataaanaataagaagaatattcaattctgaggtgaagcagagcagc 5250

QY 1139 atcatctcgtatgttctcctcagctccaattcccgaggtataaattcaaatctgaatcgagct 1198  
Db 5251 atcatctcgtatgttctcctcagctccaattcccgaggtataaattcaaatctgaatcgagct 5309

QY 1199 ctgctgctctggttggtttgaatgtagtgcagagaacagatctcagcaaacctctgaggt 1258  
Db 5310 ctgctgctctggttggtttgaatgtagtgcagagaacagatctcagcaaacctctgaggt 5369

QY 1259 aggaagctgtgctgaggttgggtgagcctcctgaggttaagggaacttaagaacaanaa 1318  
Db 5370 aggaagctgtgctgaggttgggtgagcctcctgaggttaagggaacttaagaacaanaa 5429

QY 1319 atcatctgtaattcttctcaggaagatcagagccctggagattccaagcatctgagtc 1378  
Db 1319 atcatctgtaattcttctcaggaagatcagagccctggagattccaagcatctgagtc 1378

```
Db 5430 atcatctgtaattcttctcctaagaagatcacagcccttgagatcccaagcatgagtc 5489
Qy 1379 caatctctaagaagctgctgctgactggttaattgtgtcccccctaattacatcttc 1438
Db 5490 caatctctaagaagctgctgctgactggttaattgtgtcccccctaattacatcttc 5549
Qy 1439 ttggaatctcaagctctgtgagttattttggaagaataagctctgcagatgtagttaaa 1498
Db 5550 ttggaatctcaagctctgtgagttattttggaagaataagctctgcagatgtagttaaa 5609
Qy 1499 gacaagatcatctgtgataagatgataactaatcatatgactggttccctgtatga 1558
Db 5610 gacaagatcatctgtgataagatgataactaatcatatgactggttccctgtatga 5669
Qy 1559 aaagagagagacacagacagagagagacgcgaggaagactatgtaagaatgaagacaga 1618
Db 5670 aaagagagagacacagacagagagagacgcgaggaagactatgtaagaatgaagacaga 5729
Qy 1619 gatcgagatttgcagacacaa 1640
Db 5730 gatcgagatttgcagacacaa 5751

RESULT 11
AA230052
ID AA230052 standard; DNA; 5752 BP.
AC AA230052:
XX
XX
DT 26-JUN-2000 (first entry)
DE
DE DNA encoding a human interleukin-1 receptor antagonist.
XX
XX Human: interleukin-1 receptor; IL-1; antagonist; sepsis;
XX acute pancreatitis; endotoxic shock; cytokine induced shock;
XX rheumatoid arthritis; chronic inflammatory arthritis;
XX graft versus host disease; diabetes mellitus type 1;
XX inflammatory bowel disease; autoimmune disease;
XX inflammatory disease; antiproliferative; myelogenous leukemia;
XX premature labor; intrauterine infection; nutritional activity;
XX hematopoiesis regulating activity; tissue growth activity;
XX chemokine activity; inhibin activity; chemotactic activity;
XX chemokine activity; hemostatic activity; thrombolytic activity;
XX anti-inflammatory activity; ss.
XX
XX Homo sapiens.
XX
XX MO9951744-A2.
XX
XX 14-OCT-1999.
XX
XX 05-APR-1999; 99WO-US04291.
XX
XX 03-APR-1998; 98US-0055010.
XX 15-MAY-1998; 98US-0079909.
XX 20-MAY-1998; 98US-0082364.
XX 19-JUN-1998; 98US-0099818.
XX 31-JUL-1998; 98US-0127698.
XX 13-JAN-1999; 99US-0229591.
XX 17-FEB-1999; 99US-0251370.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac R, Ctkvenjakov R, Dickson M, Drmanac S, Labat I;
XX PI Leshkowitz D, Kita D, Ford J, Pace A, Alfenito M;
XX
XX WPI; 1999-611042/52.
XX
XX New isolated interleukin-1 receptor binding polypeptides, used to treat
XX e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
XX inflammatory disease, autoimmune disease or proliferative disease
```

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PS Claim 1; Fig 9A-C; 123pp; English.
XX
XX The present sequence encodes a human interleukin-1 (IL-1) receptor
XX antagonist. It represents the genomic sequence of AA230046-51. The
XX encoded polypeptide is capable of binding IL-1 receptors (IL-1Rs). The
XX polynucleotides and polypeptides can be used for the prevention or
XX treatment of disorders involving sepsis, acute pancreatitis, endotoxic
XX shock, cytokine induced shock, rheumatoid arthritis, chronic
XX inflammatory arthritis, pancreatic cell damage from diabetes mellitus
XX type 1, graft versus host disease, inflammatory bowel disease,
XX inflammation associated with pulmonary disease, other autoimmune disease
XX or inflammatory disease, an antiproliferative agent such as for acute or
XX chronic myelogenous leukemia or in the prevention of premature labor
XX secondary to intrauterine infections. They can also exhibit activities
XX such as e.g. nutritional activity, cytokine and cell proliferation/
XX differentiation activity, immune stimulating or suppressing activity,
XX hematopoiesis regulating activity, tissue growth activity, activin/
XX inhibin activity, chemotactic/chemokinetic activity, hemostatic and
XX thrombolytic activity, receptor/ligand activity, and anti-inflammatory
XX activity. The products can also be used for detection, diagnosis and
XX drug screening.
XX
XX Sequence 5752 BP; 1467 A; 1274 C; 1489 G; 1383 T; 139 Other;
```

```
Query Match 69.5%; Score 1566.6; DB 20; Length 5752;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1624; Conservative 5; Mismatches 9; Indels 5; Gaps 5;
```

```
Qy 1 aatccaagaagcttcaacttctacacgcgagacatggagctcaactcagcttgagtcgg 60
Db 4112 aatccaagaagcttcaacttctacacgcgagacatggagctcaactcagcttgagtcgg 4171
Qy 61 cgcgcctacccgggctggttccctgtgacagtgctcctgaagccgatacctcgttaagctaa 120
Db 4172 cgcgcctacccgggctggttccctgtgacagtgctcctgaagccgatacctcgttaagctaa 4231
Qy 121 cccagcttccagagaatgtgtcgtgaatgtcccccatacaagacttctacttccagcagt 180
Db 4232 cccagcttccagagaatgtgtcgtgaatgtcccccatacaagacttctacttccagcagt 4291
Qy 181 gtgactagaggaacagctgtcccccagaactctccctgggcaagacagctgggtgaagggt 240
Db 4292 gtgactagaggaacagctgtcccccagaactctccctgggcaagacagctgggtgaagggt 4350
Qy 241 gagtgagagagacacatgagcgacaatcaactcttctgctctcagaagcccgagctca 300
Db 4351 gagtgagagagacacatgagcgacaatcaactcttctgctctcagaagcccgagctca 4410
Qy 301 cctagtgagacacttgacacttgtcttctgtgttccagcttgcataaattctgagatt 360
Db 4411 cctagtgagacacttgacacttgtcttctgtgttccagcttgcataaattctgagatt 4470
Qy 361 ggaagctcaagtcacaggtctctcccccacatgagtggtgtcactgctgtggaacctgtgaa 420
Db 4471 ggaagctcaagtcacaggtctctcccccacatgagtggtgtcactgctgtggaacctgtgaa 4530
Qy 421 accatgtgggtgaactgtgataaactgaataaagattctgtgaggggtgaggggtgaggg 480
Db 4531 accatgtgggtgaactgtgataaactgaataaagattctgtgaggggtgaggggtgaggg 4590
Qy 481 tgcctggaatcattctcgtcttaattgtaactgataaagtgttacccttgagcccgagacc 540
Db 4591 tgcctggaatcattctcgtcttaattgtaactgataaagtgttacccttgagcccgagacc 4650
Qy 541 aaccatccccaagtgagacttaagagtgtagctctccacaatgaagtcctcctcaactc 600
Db 4651 aaccatccccaagtgagacttaagagtgtagctctccacaatgaagtcctcctcctcaactc 4710
Qy 601 accactgtgcaagagagaggtgtgataagatcagagagatcagagccttgagccagc 660
Db 4711 accactgtgcaagagagaggtgtgataagatcagagagatcagagccttgagccagc 4770
```





```

QY 1 aatccaaagcttcaaccttaccgagcggaacatgaggctcaccctcagctcagatcgg 60
   |||||
Db 337 aatccaaagcttcaaccttaccgagcggaacatgaggctcaccctcagctcagatcgg 396
QY 61 ctgctaccgagctggtctctctgctcagagctgcgtaagccgatacagctctgaactca 120
   |||||
Db 397 ctgctaccgagctggtctctctgctcagagctgcgtaagccgatacagctctgaactca 456
QY 121 cccagcttcccgagaatggtggtctggaatgcccccaaccacacttcaactcagagcagt 180
   |||||
Db 457 cccagcttcccgagaatggtggtctggaatgcccccaaccacacttcaactcagagcagt 516
QY 181 gtgactagggcaacgctgcccccccaagaactccctgggacgaagccagctcgggtgaagggt 240
   |||||
Db 517 gtgactagggcaacgctgcccccccaagaactccctgggacgaagccagctcgggtgaagggt 575
QY 241 gagtgaggagagacccatctgagcggaacatcaactcttctgtctcgaagaccccgatctga 300
   |||||
Db 576 gagtgaggagagacccatctgagcggaacatcaactcttctgtctcgaagaccccgatctga 635
QY 301 cttagtgagcacttgacacacttctctctgcttccagcttgcataaattctgaacttt 360
   |||||
Db 636 cttagtgagcacttgacacacttctctctgcttccagcttgcataaattctgaacttt 695
QY 361 ggaagctagctcagaggtccctcccccacatgagatggtgactagctgctggaacctgtgaa 420
   |||||
Db 696 ggaagctagctcagaggtccctcccccacatgagatggtgactagctgctggaacctgtgaa 755
QY 421 accatgagggttaactctggaataaacaatgaataaagattcttgaggagggtgagggtgaggag 480
   |||||
Db 756 accatgagggttaactctggaataaacaatgaataaagattcttgaggagggtgagggtgaggag 815
QY 481 tgcctggaatcattccctgcttaattggttaactgaacaggtttaccctgagcccccgagccc 540
   |||||
Db 816 tgcctggaatcattccctgcttaattggttaactgaacaggtttaccctgagcccccgagccc 875
QY 541 aaccatcccgagctgagccttaatgagtgatgagctctccacatgaagctctcactca 600
   |||||
Db 876 aaccatcccgagctgagccttaatgagtgatgagctctccacatgaagctctcactca 935
QY 601 aaccagctgagagagagagaggtggtcctagatgagtcagagatctatgagcccttgagccagc 660
   |||||
Db 936 aaccagctgagagagagagaggtggtcctagatgagtcagagatctatgagcccttgagccagc 995
QY 661 cccacccccctccctt-atccctgacactgtcatgctacacttccatctctccctc 719
   |||||
Db 996 cccacccccctccctt-atccctgacactgtcatgctacacttccatctctccctc 1055
QY 720 atcaatctgtctgagcagatgagaggtggtgctgcatgctagaagaatggtctgaggtcagaa 779
   |||||
Db 1056 atcaatctgtctgagcagatgagaggtggtgctgcatgctagaagaatggtctgaggtcagaa 1115
QY 780 gataaaagataaagttaggtatgctgctctttaaataaaccgaataaataaataaatac 839
   |||||
Db 1116 gataaaagataaagttaggtatgctgctctttaaataaaccgaataaataaataaatac 1175
QY 840 ccaagatctgtctatctatcccatgaaagaatgctcatgacatctatggaagaacctactt 899
   |||||
Db 1176 ccaagatctgtctatctatcccatgaaagaatgctcatgacatctatggaagaacctactt 1235
QY 900 acaaaagtgcataatctgcaatttatttaataaagaatacctaattatatttctt 959
   |||||
Db 1236 acaaaagtgcataatctgcaatttatttaataaagaatacctaattatatttctt 1295
QY 960 atagaaaaaa 969
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Db 1296 atagaaaaaa 1305

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RESULT 13  
AAF31352  
ID AAF31352 standard; cDNA; 985 BP.

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XX AC AAF31352;
XX DT 05-APR-2001 (first entry)
XX DE B2HFLS20W cDNA library sequence #2.
XX KW Interleukin; IL-1 receptor; cancer; inflammation; ss.
XX OS Homo sapiens.
XX PN WO200102571-A2.
XX PD 11-JAN-2001.
XX PF 07-JUL-2000; 2000WO-US18710.
XX PR 07-JUL-1999; 99US-0348942.
XX PR 13-OCT-1999; 99US-0417455.
XX PR 08-DEC-1999; 99US-0457626.
XX PR 10-MAR-2000; 2000US-0523552.
XX PR 22-MAY-2000; 2000US-0576008.
XX PA (HYSE-) HYSEQ INC.
XX PI Ford J, Pace A;
XX DR WPL; 2001-071582/08.
XX PT Isolated nucleic acids encoding Interleukin-1 (IL-1) receptor
XX PT antagonist proteins (referred as IL-1H1), useful in the treatment of
XX PT cancer, e.g. breast adenocarcinoma and brain tumors, and an
XX PT inflammatory disease mediated by IL-18 -
XX PS Claim 1; Fig 2; 179pp; English.
XX CC The present invention relates to interleukin (IL)-1 receptor
XX CC antagonist proteins. IL-1H1 is useful for treating cancer,
XX CC an inflammatory disease mediated by IL-18, inflammation
XX CC resulting from infection or allergic reactions, and inflammation
XX CC associated with chronic bronchitis, arthritis, diabetes or
XX CC endohermia.
XX SQ Sequence 985 BP; 232 A; 264 C; 249 G; 240 T; 0 other;

Query Match 39.3%; Score 886.2; DB 22; Length 985;
Best Local Similarity 98.4%; Pred. NO. 4.5e-231;
Matches 916; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 aatccaaagcttcaaccttaccgagcggaacatgaggctcaccctcagctcagatcgg 60
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Db 56 aatccaaagcttcaaccttaccgagcggaacatgaggctcaccctcagctcagatcgg 115
QY 61 ctgctaccgagctggtctctctgctcagagctgcgtaagccgatacagctctgaactca 120
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Db 116 ctgctaccgagctggtctctctgctcagagctgcgtaagccgatacagctctgaactca 175
QY 121 cccagcttcccgagaatggtggtctggaatgcccccaaccacacttcaactcagagcagt 180
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Db 176 cccagcttcccgagaatggtggtctggaatgcccccaaccacacttcaactcagagcagt 235
QY 181 gtgactagggcaacgctgcccccccaagaactccctgggacgaagccagctcgggtgaagggt 240
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Db 236 gtgactagggcaacgctgcccccccaagaactccctgggacgaagccagctcgggtgaagggt 294
QY 241 gagtgaggagagacccatctgagcggaacatcaactcttctgtctcgaagaccccgatctga 300
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Db 295 gagtgaggagagacccatctgagcggaacatcaactcttctgtctcgaagaccccgatctga 354
QY 301 cttagtgagcacttgacacacttctctctgcttccagcttgcataaattctgaacttt 360
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Db 355 cttagtgagcacttgacacacttctctctgcttccagcttgcataaattctgaacttt 414

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OY 361 ggagctcaatccagggctcccccctgagatggtctactgtgtggaacctgtgtaaa 420
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DB 415 ggaagctcagatccagagctctcccccctgagatggtctactgtgtggaacctgtgtaaa 474
OY 421 accatgtggggaataacttgggaataacatgaaagattctgtgggggtgggtgggag 480
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DB 475 accatgtggggaataacttgggaataacatgaaagattctgtgggggtgggtgggag 534
OY 481 tgcctgggaatcattctctgttaactgttaactgacaaagtgttaccctggagcccgagcc 540
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DB 535 tgggtgggaatcattctctgttaactgttaactgacaaagtgttaccctggagcccgagcc 594
OY 541 aacccatcccccagttgagctataaggtcagtaagctccacatgaaatccctcaacc 600
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DB 595 aacccatcccccagttgagctataaggtcagtaagctccacatgaaatccctcaacc 654
OY 601 accactgtgcaagagagaggtgtgcatagagtcagaggaatcatalgacctgtggccagc 660
    |||||||
DB 655 accactgtgcaagagagaggtgtgcatagagtcagaggaatcatalgacctgtggccagc 714
OY 661 ccacaccccttccctt-atcctgacactgtcatatgtactcttcccttccctc 719
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DB 715 ccacaccccttccctt-atcctgacactgtcatatgtactcttcccttccctc 774
OY 720 atcatctgtgtgggcatgagaggtgtgtatgtcagagaagatggttcgagctcagaa 779
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DB 775 atcatctgtgtgtggcatgagaggtgtgtatgtcagagaagatggttcgagctcagaa 834
OY 780 gataaagaataagtaagtgatgtgtatccctctttaaaccacaaatcaatcaaatc 839
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DB 835 gataaagaataagtaagtgatgtgtatccctctttaaaccacaaatcaatcaaatc 894
OY 840 ccagatgctgtgtctatctatccatgtaaaagtgtcatatattgaaagaacctact 899
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DB 895 ccagatgctgtgtctatctatccatgtaaaagtgtcatatattgaaagaacctact 954
OY 900 acaaaatgcatatattgtcaattattttaa 930
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DB 955 acaaaatgcatatattgtcaattattttaa 985

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RESULT 14  
AAE31353  
ID AAE31353 standard: cDNA: 1282 BP.

AAE31353:

05-APR-2001 (first entry)

Extension of B2HFLS20W cDNA library sequence #2.

Interleukin: IL-1 receptor; cancer: inflammation; ss.

Homo sapiens.

WO200102571-A2.

11-JAN-2001.

07-JUL-2000; 2000MO-US18710.

07-JUL-1999; 99US-0348942.

13-OCT-1999; 99US-0417455.

08-DEC-1999; 99US-0457626.

10-MAR-2000; 2000US-0523552.

22-MAY-2000; 2000US-0576008.

(HYSE-) HYSEQ INC.  
Ford J, Pace A;  
MPI: 2001-071582/08.

```

XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor
PT antagonist proteins (referred as IL-1Hx1), useful in the treatment of
PT cancer, e.g. breast adenocarcinoma and brain tumors, and an
PT inflammatory disease mediated by IL-18.
PS Claim 1: Fig 5; 179pp; English.
XX
CC The present invention relates to interleukin (IL)-1 receptor
CC antagonist proteins. IL-1Hx1 is useful for treating cancer,
CC an inflammatory disease mediated by IL-18, inflammation
CC resulting from infection or allergic reactions, and inflammation
CC associated with chronic bronchitis, arthritis, diabetes or
CC endothelma.
XX
SQ Sequence 1282 BP; 294 A; 337 C; 350 G; 301 T; 0 other:

Query Match      39.3%; Score 886.2; DB 22; Length 1282;
Best Local Similarity 98.4%; Pred. No. 5.2e-231;
Matches 916; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

OY 1 aatccaagaagctacacctctacacggcgggacatggggtcaccctcagcttcagagtcgg 60
    |||||||
DB 353 aatccaagaagctacacctctacacggcgggacatggggtcaccctcagcttcagagtcgg 412
OY 61 ctggcctaccgggctgtgttcctgtgtcagcgtgtgtcgttaagccgactcgtgtcagactca 120
    |||||||
DB 413 ctggcctaccgggctgtgttcctgtgtcagcgtgtgtcgttaagccgactcgtgtcagactca 472
OY 121 ccgaagctcccgaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
    |||||||
DB 473 ccgaagctcccgaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 532
OY 181 gtgactaaggacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
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DB 533 gtgactaaggacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 591
OY 241 ggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
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DB 592 ggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 651
OY 301 cttaagtgagcaccctgacaccttctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
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DB 652 cttaagtgagcaccctgacaccttctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 711
OY 361 ggaagctcagatccaggttcctcccccacatgagatgtgtgtgtgtgtgtgtgtgtgtgt 420
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DB 712 ggaagctcagatccaggttcctcccccacatgagatgtgtgtgtgtgtgtgtgtgtgtgt 771
OY 421 accatgtggggaataacttgggaataacatgaaagattctgtgggggtgggtgggag 480
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DB 772 accatgtggggaataacttgggaataacatgaaagattctgtgggggtgggtgggag 831
OY 481 tgcctgggaatcattctctgttaactgttaactgacaaagtgttaccctggagcccgagcc 540
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DB 832 tgcctgggaatcattctctgttaactgttaactgacaaagtgttaccctggagcccgagcc 891
OY 541 aacccatcccccagttgagctataaggtcagtaagctccacatgaaatccctcaacc 600
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DB 892 aacccatcccccagttgagctataaggtcagtaagctccacatgaaatccctcaacc 951
OY 601 accactgtgcaagagagaggtgtgcatagagtcagaggaatcatalgacctgtggccagc 660
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DB 952 accactgtgcaagagagaggtgtgcatagagtcagaggaatcatalgacctgtggccagc 1011
OY 661 ccacaccccttccctt-atcctgacactgtcatatgtactcttcccttccctc 719
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DB 1012 ccacaccccttccctt-atcctgacactgtcatatgtactcttcccttccctc 1071
OY 720 atcatctgtgtgtggcatgagaggtgtgtatgtcagagaagatggttcgagctcagaa 779
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DB 1072 atcatctgtgtgtggcatgagaggtgtgtatgtcagagaagatggttcgagctcagaa 1131

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QY 780 gataaaagaataagtagatgctgctcctctttaaaccacgaacatacaaatc 839  
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Db 1132 gataaaagaataagtagatgctgctcctctttaaaccacgaacatacaaatc 1191  
QY 840 ccagatgctgcttccatcccatgaagaatgctccatgacatattggaagactact 899  
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Db 1192 ccagatgctgcttccatcccatgaagaatgctccatgacatattggaagactact 1251  
QY 900 acaaatgacatattgacatatttattttaa 930  
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Db 1252 acaaatgacatattgacatatttattttaa 1282

RESULT 15  
AAZ30050  
ID AAZ30050 standard; cDNA: 1282 BP.  
XX  
AC AAZ30050:  
XX  
XX 26-JAN-2000 (first entry)  
XX  
XX cDNA encoding a human interleukin-1 receptor antagonist.  
XX  
KW Human; interleukin-1 receptor; IL-1; antagonist; sepsis;  
KW acute pancreatitis; endotoxin shock; cytokine induced shock;  
KW rheumatoid arthritis; chronic inflammatory arthritis;  
KW pancreatic cell damage; diabetes mellitus type 1;  
KW graft versus host disease; inflammatory bowel disease;  
KW inflammation; pulmonary disease; autoimmune disease;  
KW inflammatory disease; antiproliferative; myelogenous leukemia;  
KW premature labor; intrauterine infection; nutritional activity;  
KW hematopoiesis regulating activity; tissue growth activity;  
KW actinin activity; inhibin activity; chemotactic activity;  
KW chemokine activity; hemostatic activity; thrombolytic activity;  
KW anti-inflammatory activity; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO951744-AZ.  
XX  
PD 14-OCT-1999.  
XX  
PE 05-APR-1999; 99MO-US04291.  
XX  
XX 03-APR-1998; 98US-0055010.  
PR 15-MAY-1998; 98US-0079909.  
PR 20-MAY-1998; 98US-0082364.  
PR 19-JUN-1998; 98US-0099818.  
PR 31-JUL-1998; 98US-0127698.  
PR 13-JAN-1999; 99US-0229591.  
PR 17-FEB-1999; 99US-0251370.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Dmanac R, Crkvenjakov R, Dickson M, Dmanac S, Labat I;  
PI Leshkowitz D, Kita D, Ford J, Pace A, Alfienito M;  
PI  
XX  
DR MPI: 1999-611042/52.  
DR  
XX  
XX P-PSDB: AAY43526.  
XX  
XX  
XX New isolated interleukin-1 receptor binding polypeptides, used to treat  
PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,  
PT inflammatory disease, autoimmune disease or proliferative disease  
XX  
XX  
PS Claim 1; Fig 5; 123pp; English.  
XX  
XX The present sequence encodes a human interleukin-1 (IL-1) receptor  
CC antagonist. The encoded polypeptide is capable of binding IL-1  
CC receptors (IL-1Rs). The polynucleotides and polypeptides can be used for  
CC the prevention or treatment of disorders involving sepsis, acute  
CC pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid  
CC arthritis, chronic inflammatory arthritis, pancreatic cell damage from

CC diabetes mellitus type 1, graft versus host disease, inflammatory bowel  
CC disease, inflammation associated with pulmonary disease, other autoimmune  
CC disease or inflammatory disease, an antiproliferative agent such as for  
CC acute or chronic myelogenous leukemia or in the prevention of premature  
CC labor secondary to intrauterine infections. They can also exhibit  
CC activities such as e.g. nutritional activity, cytokine and cell  
CC proliferation/differentiation activity, immune stimulating or  
CC suppressing activity, hematopoiesis regulating activity, tissue growth  
CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,  
CC hemostatic and thrombolytic activity, receptor/ligand activity, and  
CC anti-inflammatory activity. The products can also be used for  
CC detection, diagnosis and drug screening.  
XX  
XX  
SQ Sequence 1282 BP; 293 A; 337 C; 350 G; 301 T; 1 other;  
Query Match 39.3%; Score 885.2; DB 20; Length 1282;  
Best Local Similarity 98.3%; Pred. NO. 9.6e-231;  
Matches 915; Conservative 0; Mismatches 14; Indels 2; Gaps 2;  
QY 1 aatcaagaagcttcaactctctacccgacgagacatgagctcaactcagctcagctcgcg 60  
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Db 353 aatcaagaagcttcaactctctacccgacgagacatgagctcaactcagctcagctcgcg 412  
QY 61 ctgctaccgggctggtctcctgacagctgctgaaagccgacgctcagactca 120  
|||||  
Db 413 ctgctaccgggctggtctcctgacagctgctgaaagccgacgctcagactca 472  
QY 121 ccagcttccgagatggtgctggaatgccccatcaagacttacttccagagt 180  
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Db 473 ccagcttccgagatggtgctggaatgccccatcaagacttacttccagagt 532  
QY 181 gtaactaggagcaagctgccccccagaaactccctgagcagagccagctcgggtgaagggt 240  
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Db 533 gtaactaggagcaagctgccccccagaaactccctgagcagagccagctcgggtgaagggt 591  
QY 241 gaatgagagagaccatgaggagacaatcattctgcttccagagaccagagctga 300  
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Db 772 accatgtgggttaactggaataacatgaaagaattctgtgggggtgggtggggag 831  
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Db 1012 cccacccctccctt-ctcctgcaactgcatatgttacccttccatctccctc 1071  
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QY 780 gataaaagaataagtagatgctcctctttaaaccacgaacatacaaatc 839

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Oy 840 ccagatgctgtgtctctatcccaatgaataaagtgcacatgacatatggagaagactactt 899
Db 1192 ccagatgctgtgtctctatcccaatgaataaagtgcacatgacatatggagaagactactt 1251
Oy 900 acaagtgacatatatgcaattttaa 930
Db 1252 ncaagtgacatatatgcaattttaa 1282
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Search completed: March 1, 2002, 11:57:07  
Job time: 3267 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2002, 10:15:34 ; Search time 1181.65 Seconds  
(without alignments)  
20488.503 Million cell updates/sec

Title: US-09-617-720-1\_COPY\_310\_2562

Perfect score: 2253

Sequence: 1 aatcaagagcttcacaccc.....aatatatacgagaaag 2253

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues  
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:  
1: em\_estfun:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estcom:  
5: em\_estpl:  
6: em\_estba:  
7: em\_estro:  
8: em\_estov:  
9: em\_hc:  
10: gb\_estcl:  
11: gb\_estcl:  
12: gb\_hc:  
13: gb\_gss:  
14: em\_gss\_fun:  
15: em\_gss\_hum:  
16: em\_gss\_inv:  
17: em\_gss\_pln:  
18: em\_gss\_pro:  
19: em\_gss\_rnd:  
20: em\_gss\_vrt:  
21: em\_gss\_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	978.6	43.4	1011	10	AL570964
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4	527.8	23.4	555	10	AL570964
5	465	20.6	467	13	AL570964
6	451.2	20.0	485	10	AL570964
7	435.8	19.3	464	11	AL570964
8	426.8	18.9	464	10	AL570964
9	417	18.5	442	10	AL570964
10	413.8	18.4	726	11	AL570964
11	404	17.9	932	10	AL570964
12	398.2	17.7	414	10	AA722902

c 13	393.6	17.5	435	10	BE711845
c 14	387.4	17.2	410	10	AL167887
c 15	380.8	16.9	416	10	AL157708
c 16	349.6	15.5	400	11	BG010066
c 17	349.4	15.3	374	11	R70041
c 18	322.6	14.3	858	11	B1090567
c 19	315.4	14.0	348	11	R70089
c 20	222	9.9	235	10	AM014217
c 21	161.6	7.2	2843	12	AK014576
c 22	156.4	6.9	1051	12	AK009741
c 23	156.4	6.9	1199	12	AK008977
c 24	156.4	6.9	1531	12	AK010020
c 25	152	6.7	459	13	AK011498
c 26	143.6	6.4	589	13	AK047870
c 27	141.6	6.3	355	10	AL192214
c 28	139.2	6.2	396	10	AA044669
c 29	137.8	6.1	480	10	AA699597
c 30	137.2	6.1	453	10	AL1217140
c 31	134.2	6.0	425	10	AA884631
c 32	134.2	6.0	620	13	AK0581771
c 33	132.8	5.9	625	13	AK080752
c 34	132.2	5.9	522	13	AK0412751
c 35	132	5.9	762	13	AK036188
c 36	131	5.8	395	10	AK665185
c 37	128.6	5.7	432	10	AK015963
c 38	128.6	5.7	509	13	AK092917
c 39	127.4	5.7	720	10	AV06704
c 40	125.8	5.6	546	10	AV720202
c 41	125.6	5.6	475	13	AK0707306
c 42	125.4	5.6	621	13	AK0379758
c 43	125.4	5.6	659	13	AK0485265
c 44	125.2	5.6	364	11	BF802657
c 45	123	5.5	370	13	AK518945

## ALIGNMENTS

RESULT 1  
BC000945  
LOCUS BC000945 1648 bp mRNA HTC  
DEFINITION Homo sapiens, clone IMAGE:3447369, mRNA.  
ACCESSION BC000945  
VERSION BC000945.2 GI:14705316  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2000) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
On Jul 12, 2001 this sequence version replaced gi:13937574.  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [villalobom@bcm.tmc.edu](mailto:villalobom@bcm.tmc.edu)  
Villalobon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found







driver population), a pool of clones from NCI\_CGAP\_Sub4 (IMAGE clone ids 2723592-2729326; 25% of the driver population), NCI\_CGAP\_Sub6 (pool AIR-AU, IMAGE ids 2728969-2733190; 25% of the driver population), and NCI\_CGAP\_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described (Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG\_LIB=NCI\_CGAP\_LuJ9

TAG\_TISSUE=lung

TAG\_SEQ=GACACG

BASE COUNT 190 a 154 c 160 g 192 t 1 others

ORIGIN

Query Match 28.5%; Score 643.2; DB 11; Length 697;

Best Local Similarity 97.7%; Pred. No. 2e-130; Mismatches 14; Indels 2; Gaps 2;

Matches 673; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

```

282 tcaggacccccagctctacttagtgggacacttaccacattgtctctgttccagtt 341
|||||
697 tcaggacccccagctctacttagtgggacacttaccacattgtctctgttccagtt 638
|||||
342 tcgataaattctgagatttggagctcagtcagggtctccccacactgagatgtctact 401
|||||
637 tggatgaattctgagatttggagctcagtcagggtctccccacactgagatgtctact 579
|||||
402 gctgtggaaccttgaataaacacatgtgggttaaacctgggaaataacatgaaagattctg 461
|||||
578 gctgtggaaccttgaataaacacatgtgggttaaacctgggaaataacatgaaagattctg 519
|||||
462 tgggggtgggggtgggggtgctctggaatactctctcttaataatgtaacagacagttgt 521
|||||
518 tggagagtgagggtgggggtgctctggaatactctctcttaataatgtaacagacagttgt 459
|||||
522 accctgagccccagcagcgaacccaatcccaagtgaagcctataaggttcagtagctc 581
|||||
458 accctgagccccagcagcgaacccaatcccaagtgaagcctataaggttcagtagctc 399
|||||
582 acatgaagtcctctactcaccacactgtgcaagagaagaggtgtgtcatagagtcagagat 641
|||||
398 acatgaagtcctctactcaccacactgtgcaagagaagaggtgtgtcatagagtcagagat 339
|||||
642 ctatgaccttggcccaagccccacccctccctt-atcctgcaactgcatatgctac 700
|||||
338 ctatgaccttggcccaagccccacccctccctt-atcctgcaactgcatatgctac 279
|||||
701 ctctccatctctctccatcatctgtgtgtggaatggaaggtgtgtgtcagaag 760
|||||
278 ctctccatctctctccatcatctgtgtgtggaatggaaggtgtgtgtcagaag 219
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761 aaatggttcgagctagaagaataagaataagtaggtatgtgtgtatccctctttaaagac 820
|||||
218 aaatggttcgagctagaagaataagaataagtaggtatgtgtgtatccctctttaaagac 159
|||||
821 ccaagatacaatacaaatcccaagatgtgtgtgtatccatccatgaaaggtgtcagagac 880
|||||
158 ccaagatacaatacaaatcccaagatgtgtgtgtatccatccatgaaaggtgtcagagac 99
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881 atattgagaagaactactatacaagttgcatatattgcaatttattttaaataaagata 940
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98 atattgagaagaactactatacaagttgcatatattgcaatttattttaaataaagata 39
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941 cctatttatataattctcttatagaataa 969
|||||
38 cctatttatataattctcttatagaataa 10
|||||

```

RESULT 4  
AUI38695 555 bp mRNA EST 25-OCT-2000

DEFINITION AUI38695 PLACE1 Homo sapiens cDNA clone PLACE1009110 5', mRNA sequence.

ACCESSION AUI38695

VERSION AUI38695.1 GI:11000216

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saijo,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and





QY	865	aaaaagggccatgcaacatcttgggaagagccctacttcaaaagctgcatatctgcaattt	924
Db	481	AAAAAAAAAGGTCATGACATATTGAMAANACCTACTTCAAAAGTGCGATATTATTTGCAATTTA	540
QY	925	tttaattaaaagat	939
Db	541	TTTTTAATTTAAAGAT	555
RESULT	5		
AS521126			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			
BASE COUNT			
ORIGIN			
Query Match	20.68;	Score 465;	DB 13; Length 467;
Best Local Similarity	99.68;	Pred. No. 2e-91;	
Matches 465; Conservative	0;	Mismatches 2;	Indels 0; Gaps 0
QY	1203	tgacctggttggtgtgtagtagtagatcagaagaacagctcagaacaagccacgaggaaga	1262
Db	1	TGCTCTGTTGGTTGTAGTAGTATGCGGAAGAAAGATCTACGCAAGGCCACTGACGAGAGA	60
QY	1263	ggctgtgctgagattgtgtggtcctggaatctcttggctaaagaaacttaagaacaaaaatca	1322
Db	61	GGCTGTGCTGCTAGATTGTGTGCTGCGATGCTCTGCTGGTAAGAACTTAAGAAACAAATAATCA	120
QY	1323	tcgtgtaatccttctcagaagaagatacaagcccccttgagattccaaggaattgataccagt	1382

Db	121	TCTGGTATTTCTTCTTCTGAAGATCACAGCCCTCGNATTTCCAAAGCATTTGGATCCAGT	180
Oy	1383	ctctaaagaagccctgctgactggttgaattgltgccccccaatlcacatcctcttgg	1442
Db	181	CTCTAAGAAGGCTGCTGACTGTTGAATTTGTGCCCTCAAAATTCACATCTCTTGG	240
Oy	1443	aatccagtcgtgagttattcttgagataaagtcctcgcagatgtagttagttaaagaca	1502
Db	241	AATCTCACTCTCTGTGATTATTTGGAGATTAAGGTCCTCGCAGATGTACTTAAGTAAAGCA	300
Oy	1503	aggtcatcctgataaaggtagacctaatcacaatgactggttccctctgtaagaaag	1562
Db	301	AGGTCACTCTGTGATGTAAGGTAGACCTTAATTCATATGACTGTTTCTTTATGAAAG	360
Oy	1563	gagagagacacagagacagagagacgcgagggaagactatgtaaaagatgaagcagagatc	1622
Db	361	GAGAGACACAGACAGACAGAGAGACGCGNAGACACTATGTAAGATGAAGCAGAGATC	420
Oy	1623	ggagatttgcagcccaagcctaaagaacacccaagaagtgtggcaac	1669
Db	421	GGAGTTTTCAGCCCAAGCTAAGAAACCCAGAGATTGTGGCAAC	467

RESULT 6

LOCUS A1040890/c

DEFINITION A1040890 485 bp mRNA EST 28-AUG-1998

ACCESSION ow26a12.x1 Soares-parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone

VERSION IMAGE:1647934.3, mRNA sequence.

KEYWORDS A1040890 A1040890.1 GI:3280084

SOURCE EST.

ORGANISM human.

human.

Human sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.

1 (bases 1 to 485)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html

Insert Length: 1417 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 473.

Location/Qualifiers

1. 485

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1647934"

/clone\_lib="Soares parathyroid\_tumor\_NbHPA"

/tissue\_type="parathyroid tumor"

/dev\_stage="adult"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: parathyroid gland; Vector: pRT73D (Pharmacia RI) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

15-TGTTACCAATCTGAGTGGAGCGCCGACACCAATTTTTTTTTTTTTTTTTTTT

TTTTT-71', double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid



REFERENCE 1 (bases 1 to 464)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
JOURNAL Tumor Gene Index  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Emmett Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrrp/image/image.html  
Insert length: 848 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 433.  
Location/Qualifiers  
1. 464  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:240572"  
/clone\_11b="NCI-CGAP\_Lu19"  
/tissue\_type="squamous cell carcinoma, poorly  
differentiated (4 pooled tumors, including primary and  
metastatic)"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: Lung; Vector: pPT73D-Pac (Pharmacia) with a  
modified polylinker; 1st strand cDNA was prepared from  
pooled lung tumor tissue, and was then primed with a Not I  
- oligo(dT) primer. Double-stranded cDNA was ligated to  
Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pPT73 vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 128 a 94 c 104 g 138 t  
ORIGIN

Query Match 18.9%; Score 426.8; DB 10; Length 464;  
Best Local Similarity 98.2%; Pred. No. 4.5e-83;  
Matches 442; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Q 1804 ccaagataaattggtctacagcagctctagaagaactaacagctgctaaatgaatccctg 1863  
|||||  
D 464 ccaagataaattggtctacagcagctctagaagaactaacagctgctaaatgaatccctg 405  
|||||

Q 1864 tctctctggttctacatctgtgtgtgtccctcccaaatgataaagttctctgt 1923  
|||||  
D 404 tctctctggttctacatctgtgtgtgtccctcccaaatgataaagttctctgt 345  
|||||

Q 1924 gaccacaataagatgagagaagtgatgacatgacactccaagaattagttataaaga 1983  
|||||  
D 344 ga-ccatagatgataatgacagagatgacatgacactccaagaattagttataaaga 286  
|||||

Q 1984 caatgacgctctacttgaagccctctctctgcaaccacaccccccacatctctg 2043  
|||||  
D 285 cactgacgctctacttgaagccctctctctgcaaccacaccccccacatctctg 226  
|||||

Q 2044 ctactgctctctgaggaagatgacatgacatgacagagcctataaagaactaac 2103  
|||||  
D 225 ctactgctctctgaggaagatgacatgacatgacagagcctataaagaactaac 166  
|||||

Q 2104 gtagtaaaaaatgaagtcctgcccacagacacattagtaacctagaacagagctc 2163  
|||||  
D 165 gtagtaaaaaatgaagtcctgcccacagacacattagtaacctagaacagagctc 106  
|||||

Q 2164 tctgagaaatcgaatgcttctgtttaaagttgctcagtttggcttaactgtatga 2223  
|||||

Db 105 TGTGAGATATCATGATGTTTGTGTTTAACTTGCTACATTGTCATACCTGTTATGCA 46  
Q 2224 gcaatagataataatataatgacagagaagag 2253  
|||||  
D 45 GCAATAGATATATATATATGACAGAGAAAGAG 16  
|||||

RESULT 9  
LOCUS A1469873/c 442 bp mRNA EST 14-APR-1999  
DEFINITION U788a08.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P.S1 Homo sapiens cDNA clone  
IMAGE:2148566 3', mRNA sequence.  
ACCESSION A1469873  
VERSION A1469873.1 GI:4331963  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 442)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
JOURNAL Tumor Gene Index  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 610 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 437.  
Location/Qualifiers  
1. 442  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2148566"  
/clone\_11b="Soares\_NSF\_F8\_9W\_OT\_PA\_P.S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pPT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from five normalized  
libraries were mixed, and ss circles were made in vitro.  
Following HAP purification, this DNA was used as tracer in  
a subtractive hybridization reaction. The driver was  
PCR-amplified cDNAs from pools of 5,000 clones made from  
the same 5 libraries. The pools consisted of the following  
libraries and clones: Soares NBHF pool 1:  
309384-310919, 323208-325895 Soares NB2HP pool 1:  
145032-147335, 147720-148103, 148872-149255, 15002 -  
150407, 151176-152337 Soares NB2HP-9W pool 1:  
758280-760583, 772104-774407 Soares NBHP pool 1:  
304776-306311, 320136-322823, 326280-326663 Soares NBHF  
pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 119 a 89 c 102 g 132 t  
ORIGIN

Query Match 18.5%; Score 417; DB 10; Length 442;  
Best Local Similarity 99.8%; Pred. No. 6.2e-81;  
Matches 428; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Q 1825 agctctggaataataacagctgtaaaatgacccgctctcgtgttatactctg 1884  
|||||  
D 442 AGCTCTAGGAACATTAATACCTGCTAAATGATCCCTGCTCGTGTATCAATCTG 383  
|||||

Q 1885 tctgtccctcccaaatgtacaaagtgtctcttgcacccaatgaatcagcaga 1944  
|||||  
D 382 TGTGTGTCCTCCACAGATGTACCAAGTGTCTTTGTGA-CCATATGATATAGGAGCA 324  
|||||

Q 1945 agtagtgacatgacactccaagataggtatataaagacacagctctactgagc 2004  
|||||  
D 323 AGTGATGACATGCCACTTCCAAAGATTAGTTAAAGACACTGACACTTACTTGAGC 264  
|||||

QY 2005 cctctctctcgtccacccacgcccccaatctatcttggctcactcgctctgggggaagc 2064  
|||||  
DB 263 CCTCTCTCTCTGCGACACCGCCGCCCAATCTGCTGCTCACTCGCTGGGGGAGC 204  
QY 2065 tagctgcacatgctatgagcagagcctataaagaagacttaagtgtaaaaatgaagctcc 2124  
|||||  
DB 203 TGGCTGCCCTGCTATGACGAGCCCTATTAAGAGACTTACGCTGTAATAAATGAAGTCTCC 144  
QY 2125 tcccccaacacacatagtgaaacctagaagacagagactctgtgataatcgaatgttgc 2184  
|||||  
DB 143 TCCCCACAGCCCATTTAGTAACCTAGACGAGACTCTGTGATTAATCGATGTTTGT 84  
QY 2185 tgttttaagtgtcagcttggcttaactgtgtatgcaagaatagaataatagca 2244  
|||||  
DB 83 TGTTTTAAGTCTCAGTTTGTGCTTACTTGTATGCAATAATGATATATATATGCA 24  
QY 2245 gaggaaagag 2253  
|||||  
DB 23 GAGAAAGAG 15

RESULT 10  
LOCUS B1089828 726 bp mRNA EST 20-JUN-2001  
DEFINITION 60285071P1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:496432 5',  
mRNA sequence.  
ACCESSION B1089828  
VERSION B1089828.1 GI:14508158  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 726)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
Plate: L1AM1021 row: n column: 17  
High quality sequence stop: 709.  
Location/Qualifiers  
1..726  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:496432"  
/clone\_lib="NIH\_MGC\_10"  
/cell\_line="MGC36"  
/lab\_host="DH10B"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5 kb. Library prepared by Life  
Technologies."

BASE COUNT 151 a 201 c 213 g 161 t  
ORIGIN

Query Match 18.4% Score 413.8; DB 11: Length 726;  
Best Local Similarity 96.9%; Pred. No. 3e-80;  
Matches 443; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 1 aatccaagagctcacctctacacgagcgagacatgagcgctcaccctcagctcagtcgagc 60  
|||||  
DB 271 ATCCAGAGCTTCACTTCTACCGCGGACATGGGGCTCACCCTCCAGCTTGAGTGG 330

QY 61 ctgctaccggygctggtctccgtgcaaggtgacctgaagccgaatcagcctgcaagctca 120  
|||||  
DB 331 CTGCTACCCCGGGCTGGTCTCTGACAGGTCCTGAAGCCGATCAGCTGTGACACTCA 390  
QY 121 cccagctcccgagagatggtgctggaatgcccccaatcaagaagcttctacttcagcagt 180  
|||||  
DB 391 CCCAGCTTCCGAGAAAGTGTCGGAATGCCCCCAACACAGACTTCTACTTCACACAGT 450  
QY 181 gtgaatgagcaagctgccccccagaaacctccctgtggcagaagcagactcggtggaagg 240  
|||||  
DB 451 GTGACTAGGGAACAGTGC-CCCCCAGAACTCCCTGGGCAAGACCCAGCTCGGGTGA 509  
QY 241 gagtgaagagaccatgagcggaacaatcactcttctgctctcaaggacccccagtcga 300  
|||||  
DB 510 GAGTGAGAGAACCCATGCGGACATCATCTCTGCTCAGGACCCCGACGTCGA 569  
QY 301 cttagtgggaccccgacacacttcttctggttcccaagttgcaataatctggaatt 360  
|||||  
DB 570 CTTAGTGGGACCTGACACACTTGTCTGTCGCCAGTATGGAATATCTGAGATATT 629  
QY 361 gtagctcagtcagggtcct-ccccactgagatggtgctactgctgtggaactgtgaa 419  
|||||  
DB 630 GGAGCTCAGCTCAGCGTCTACCCCACTGGATGCTCTGCTGCAACCTTTTAA 689  
QY 420 aaccatgtggtggttaactgtggaataacatgaaagat 456  
|||||  
DB 690 AACCATGTGGGTAAACTGGGAATCACCCTGAAGAAGAT 726

RESULT 11  
LOCUS AL545100 932 bp mRNA EST 16-FEB-2001  
DEFINITION AL545100 LTI\_NFL006\_P12 Homo sapiens cDNA clone CS0D1013YA07 5  
prime, mRNA sequence.  
ACCESSION AL545100  
VERSION AL545100.1 GI:12877581  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 932)  
L.I.W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1..932  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0D1013YA07"  
/clone\_lib="LTI\_NFL006\_P12"  
/tissue\_type="placenta"  
/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 206 a 230 c 290 g 201 t  
ORIGIN

Query Match 17.9% Score 404; DB 10: Length 932;  
Best Local Similarity 94.4%; Pred. No. 4.2e-78;  
Matches 459; Conservative 3; Mismatches 18; Indels 6; Gaps 4;



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QY 1 aatccaaagagcttacccttaccgagcgagacatgagggctaccctcagcttcgagtcg 60
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Db 375 AATCCAAAGAGCTTACCTTCTACCGCGGCGACATGGGCTACCTCCAGCTTCGAGTGG 434
QY 61 ctgcctaccgagcttggtctcctgctgcacggtgctcgaagccgacagctgctcagactca 120
    |||||||
Db 435 CTGCGTACCGCGGCTGGTCTCTGTGACAGGTGCTGAAAGCCGATCAGCTGTGACAGTCA 494
QY 121 cccagcttcccgagaaatggtgctggaatgcgcccaatcaagaacttctacttccagcagt 180
    |||||||
Db 495 CCCAGCTTCCCGAGAAATGCTGTGGAATGCCCATCACAGACTTCTACTTCCAGCAGCT 554
QY 181 gtgactgaggaacggtgccccccagaaactcctcgagagagcagcagctcgagagagt 240
    |||||||
Db 555 GTGACTAGGGACAGGTG-CGCCCCAGAACTCCCTGGGAGAGCCAGCTCGGGGTAGGGGT 613
QY 241 gagtggaggaagaccatgagcggaacatcactcttctgctcagagaccacaggtctga 300
    |||||||
Db 614 GAGTGGAGAGACCCCATGGCGGACATCATCTCTCTCTCTCTCAGAGACCCCGAGTCTGA 573
QY 301 ctctgtggagcctgacacacttctctctgctccagcttgcataatctcagactt 360
    |||||||
Db 674 CTGAGTGGGCA-CTGACCACTTGTCTGTCTGCTCCAGTTGGATTAATCTGAGATT 732
QY 361 ggaactcagctcagaggtcctcccccacatgagtggtgctgactgctgagagcctgtaaaa 420
    |||||||
Db 733 GGACTCATGCTCAGCGGTCTCCCTCCACTGATGCTGCTACTGCTGTGGAACCTTGT-AAA 791
QY 421 accatgtggggtaaacctggaataacatgaaagaattctgttgagggtgagggag 480
    |||||||
Db 792 ACCATGTGGGGTAACTGGGATTA--TGAAAGATTCTGTGGGGGTGGGGGGGRT 848
QY 481 tgcctg 486
    ||
Db 849 GGTGGG 854

RESULT 12
LOCUS AA722902/c 414 bp mRNA EST 02-JAN-1998
DEFINITION 2881a03.s1 Soares_fetal_heart_NBHI19W Homo sapiens CDNA clone
IMAGE:399724 3', mRNA sequence.
ACCESSION AA722902
VERSION AA722902.1 GI:2740609
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S.,
Kitzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,
J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE Mashu-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 401.
FEATURES
SOURCE Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:399724"
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/sex="unknown"
/idev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pRT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAGTGGGCGGCGCATCTTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHI19W."
BASE COUNT 119 a 83 c 98 g 114 t
ORIGIN
Query Match 17.7% Score 398.2; DB:10; Length 414;
Best Local Similarity 99.0% Pred. No. 8.1e-77;
Matches 411; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1833 gaaactaatcagctgcacaaatgatccctgctcctcgtgttaccattcgtgtgtc 1892
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Db 414 GAACTAATACAGCTGCTAAATGATCCCTGTCTCTCTGTATTAATCTGTGTGTTC 355
QY 1893 cctccccaaatgtaacaaatgctctgtgacccaatagaatatggcagaagtgatgg 1952
    |||||||
Db 354 CCTCCCAATGTAACCAAACTGCTTGTGTA-CCAATAGAAATGCGACAAGATGATG 296
QY 1993 catgcaacttccaagatagttataaagacacgcagcttctactgaacctcttc 2012
    |||||||
Db 295 CATGCCACTTCCAGATTAGTGTATTAAGACACTGCACTTCTACTGACCCCTCTTC 236
QY 2013 tctgcaccaccccccacatctatctgtgctcactcgcctcgaggagagctagtcgc 2072
    |||||||
Db 235 TCTGCCACCCACCGCCCATATCTATCTTGCTGCTACTGCTGTGGGGAAGACTGACTTC 176
QY 2073 atgctatgagcagcctataaagagacttgcgtgtaaaaaatgaagtcctcccca 2132
    |||||||
Db 175 ATGCTATGAGCAGCGCTTAAAGACTTATGTGTAATAAATGAAGTCTCTCCGCCACA 116
QY 2133 gccacatagtgaaacctgaagcagagactctgtgagataatcgatgttgttttaa 2192
    |||||||
Db 115 GCCACATTATGTAACCTTGAAGCAGACTCTGTGATTAATCAATGTGTTTAA 56
QY 2193 gttgctcagcttgtctcaactgtgtacgagcaataaataataatgacagag 2247
    |||||||
Db 55 GTTGCTCAGTTTGTGCTTACTTGTATGACAGCAATACATTAATATATGCGACAG 1

RESULT 13
LOCUS BE711845/c 435 bp mRNA EST 12-SEP-2000
DEFINITION QW2-HIT0698-070700-264-h07 HIT0698 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE711845
VERSION BE711845.1 GI:10100110
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zaio,M.A., Bordoli,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
```



QY 801 gctgacccctctttaaaccacaagatacaataaaatccagatgctgtctatcc 860  
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 Db 170 GCGATCCTCTTTAAACCACAGATACATATAATCCACATGCTGCTCTATTC 111  
 QY 861 catgaaagatgctcatgacatactgagaagacctacttaagaatgagcatatgcaa 920  
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 Db 110 CAGCAAAAGCTCCTACATATGAGAGACCTACTTACAAAGTGGCATATATTCGAA 51  
 QY 921 ttattttaaataagataccattatataattcttcttaaaaaa 969  
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 Db 50 TTTATTTTAAATTAAGATACCTATTTATATTTCTTATAGAAAAA 2

## RESULT 15

LOCUS AUI57708 416 bp mRNA EST 25-OCT-2000  
 DEFINITION AUI57708 PLACE1 Homo sapiens cDNA clone PLACE1009110 3', mRNA  
 sequence.

ACCESSION AUI57708  
 VERSION AUI57708.1 GI:11019229  
 KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo:  
 1 (bases 1 to 416)  
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,  
 Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,  
 S. and Isogai,T.).

## TITLE

HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S.,  
 Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura  
 Y., Nagai,T., Sugano,S., Isogai,T.)

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3951  
 Fax: 81-438-52-3952  
 Email: genomics@hri.co.jp  
 HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix  
 Research Institute: cDNA library construction: Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.

## FEATURES

Location/Qualifiers

1..416  
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 /db\_xref="taxon:9606"  
 /clone="PLACE1009110"  
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 /issue\_type="placenta"  
 /note="Vector: pME18SFL3"

BASE COUNT 118 a 86 c 82 g 117 t 13 others

## ORIGIN

Query Match 16.9%; Score 380.8; DB 10; Length 416;  
 Best Local Similarity 95.0%; Pred. No. 5.2e-73;  
 Matches 396; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 1835 aactaatagcagctgaataatgataccctgctcctgctgcttactatcgtgtgtcc 1894  
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 Db 416 AATATATACAGNTGNTAAANGATCCNTGTTCTTGCTGTAACATTTCTGTGTGCC 357  
 QY 1895 ctccacaatgataccaagtgtctctgtgacccaatagataatgagagaagtgtatgca 1954  
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 Db 356 CTCACCAATGATGACAAAGTTGTTTGTGA-CCAATGAAATATGCGAAGTGTATGCA 298  
 QY 1955 tgcacactcaagaattaggtataaagaacacgtcagcttacttgaagccctctctc 2014  
 |||  
 Db 297 TGCACACTTCACAAAGATTAGTTATAAAGACATGACAGNTTTTACTTGAGCCCTTTT 238

QY 2015 tgcaccacacgcccccaatctactgtgctcaactcgtctctggtggggaagctagctgcat 2074  
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 Db 237 TGCACACACAGCCGCCCAATNTATCTTGCTGCTACCTGCTGCGGAGCTAGCTGCAT 178  
 QY 2075 gctatgacagagcctataaagaagacttaagctggtgaaanaa tgaagctcctgcccacagc 2134  
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 Db 177 GCTATGAGCAGGCTATTAAGAGACTTACGTGCTAAATAATGAAGTNTCTGCCACAGC 118  
 QY 2135 cacattagtgaaactgaagcagaagactctgtgaagtaacgaatgttctgttctaagc 2194  
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 Db 117 CACATTAGTGAACCTAGAACGACAGANTCTGTGAGATTAATCGATGTTGTGTTTAAGT 58  
 QY 2195 tgcacagcttctgctcaactgtctatgcaagcaatagaataaataatgacagaaaag 2251  
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 Db 57 TGCTCACTTTTGCTTACTTGTATGACGACATAGATAATATATATGACAGAAAG 1

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